



# **STIC Search Report**

## **Biotech-Chem Library**

**STIC Database Tracking Number: 123264**

**TO: Michael Borin**  
**Location: REM-2A55&2C70**  
**Art Unit: 1631**  
**June 2, 2004**  
  
**Case Serial Number: 09/854906**

**From: P. Sheppard**  
**Location: Remsen Building**  
**Phone: (571) 272-2529**  
  
**sheppard@uspto.gov**

### **Search Notes**

STIC-Biotech/ChemLib

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From: Borin, Michael  
Sent: Friday, May 28, 2004 4:39 PM  
To: STIC-Biotech/ChemLib  
Subject: Search request: 09/854906

123264

Examiner: M.Borin  
AU: 1631  
Mailbox:2C70  
Office: Remsen 2A55  
Tel.: 20713

CKFE

RE: 09/854906; TNFR-1

---

Please conduct search of polypeptide SEQ ID 1,8,9 against the commercial protein database.

Thank you

Searcher: \_\_\_\_\_  
Phone: \_\_\_\_\_  
Location: \_\_\_\_\_  
Date Picked Up: \_\_\_\_\_  
Date Completed: \_\_\_\_\_  
Searcher Prep/Review: \_\_\_\_\_  
Clerical: \_\_\_\_\_  
Online time: \_\_\_\_\_

TYPE OF SEARCH:  
NA Sequences: \_\_\_\_\_  
AA Sequences: \_\_\_\_\_  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST (where applic.)  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 1, 2004, 14:30:06 ; Search time 48.9581 Seconds  
(without alignments)  
646.376 Million cell updates/sec

Title: US-09-854-906-1  
Perfect score: 587  
Sequence: 1 MAHKPQSLDTPATLVAVV.....DIEALCGPAALPPAPSLR 112

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : A\_Geneseq\_29Jan04:\*
- 1: geneseqp1980s:\*
  - 2: geneseqp1990s:\*
  - 3: geneseqp2000s:\*
  - 4: geneseqp2001s:\*
  - 5: geneseqp2002s:\*
  - 6: geneseqp2003as:\*
  - 7: geneseqp2003bs:\*
  - 8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	587	100.0	112	5	ABB81751	Abb81751 Tumour ne
2	579	98.6	111	5	ABB81749	Abb81749 Tumour ne
3	579	98.6	158	5	ABG70127	Abg70127 Human pre
4	579	98.6	426	7	ABW00828	Abw00828 Human p55
5	579	98.6	453	4	AAB50895	Aab50895 Human TNF
6	579	98.6	455	2	ABG74755	Abg74755 Human TNF
7	579	98.6	455	2	AAR07451	Aar07451 Human Tum
8	579	98.6	455	2	ABG74751	Abg74751 Human TNF
9	579	98.6	455	2	AAR12550	Aar12550 Type I TN
10	579	98.6	455	2	AAR10986	Aar10986 30kD TNF
11	579	98.6	455	2	AAR11082	Aar11082 Human 55k
12	579	98.6	455	2	AAR20787	Aar20787 TNF-alpha
13	579	98.6	455	2	AAR42059	Aar42059 Lambda de
14	579	98.6	455	2	AAR51034	Aar51034 Mutant p5
15	579	98.6	455	2	AAR42197	Aar42197 p55 Tumou
16	579	98.6	455	2	AAR75084	Aar75084 p55 TNF-R
17	579	98.6	455	2	AAY30934	Aay30934 Human tum
18	579	98.6	455	3	AAB01336	Aab01336 TNF-R1 de
19	579	98.6	455	3	AAB26984	Aab26984 Human TNF
20	579	98.6	455	3	AAB36266	Aab36266 Human tum
21	579	98.6	455	3	AAB23446	Aab23446 Human tum
22	579	98.6	455	3	AAB37800	Aab37800 Human tum
23	579	98.6	455	4	AAB86817	Aab86817 Human TNF
24	579	98.6	455	4	AAB37677	Aab37677 Human 30
25	579	98.6	455	4	AAB36697	Aab36697 Human tum

26	579	98.6	455	5	AAU75064	Aau75064 Human tum
27	579	98.6	455	5	AAO22286	Aao22286 TNFR1 exp
28	579	98.6	455	5	ABB81649	Abb81649 Human tum
29	579	98.6	455	5	ABP54799	Abp54799 Human COP
30	579	98.6	455	6	ABP70914	Abp70914 Human CON
31	579	98.6	455	6	ABR58539	Abr58539 Human tum
32	579	98.6	455	6	ADA20581	Ada20581 Precursor
33	579	98.6	455	7	ADE57929	Ade57929 Human Pro
34	579	98.6	909	2	AAW64485	Aaw64485 Human Fas
35	554	94.4	455	2	AAR24000	Aar24000 TNF-alpha
36	518	88.2	443	2	AAR51033	Aar51033 Mutant p5
37	466	79.4	433	2	AAR51032	Aar51032 Mutant p5
38	443	75.5	86	4	AAAY97655	Aay97655 Human TNF
39	443	75.5	108	2	AAW73570	Aaw73570 Cytoplasm
40	421	71.7	471	5	ABB98169	Abb98169 Bovine tu
41	421	71.7	471	5	AAE25816	Aae25816 Bovine tu
42	404	68.8	78	5	ABG31493	Abg31493 Human Apo
43	404	68.8	78	6	ADA49709	Ada49709 Death dom
44	394.5	67.2	84	2	AAW62179	Aaw62179 Tumour ne
45	384	65.4	461	2	ABG74754	Abg74754 Rat TNF-R

ALIGNMENTS

RESULT 1  
ABB81751  
ID ABB81751 standard; protein; 112 AA.  
XX  
AC ABB81751;  
XX  
DT 10-SEP-2002 (first entry)  
XX  
DE Tumour necrosis factor receptor 1 death domain (longer sequence).  
XX  
KW Tumour necrosis factor receptor 1; receptor; TNFR-1; death domain;  
KW receptor signalling; TNFR-1 DD; protein co-ordinate data.  
XX  
OS Unidentified.  
XX  
PN US2002045578-A1.  
XX  
PD 18-APR-2002.  
XX  
PF 14-MAY-2001; 2001US-00854906.  
XX  
PR 22-MAY-2000; 2000US-0206215P.  
XX

(SUKITS) SUKITS S F.  
(XUGG/) XU G.  
(LINL/) LIN L.  
(TELL/) TELLIEZ J.  
(HSUS/) HSU S.

Sukits SF, Xu G, Lin L, Telliez J, Hsu S;  
WPI; 2002-443412/47.

Solution comprising tumor necrosis factor receptor 1 death domain, useful for identifying potential inhibitor of tumor necrosis factor receptor 1 death domain.

Claim 1; Fig 7; 49pp; English.

The sequence represents the tumour necrosis factor receptor 1 death domain (TNFR-1 DD), which is the intracellular functional domain responsible for the receptor signalling activities. The invention relates to a novel solution comprising a tumour necrosis factor receptor 1 death domain. The solution is useful for identifying a potential inhibitor of TNFR-1 DD, for the design and selection of potent and selective inhibitors of TNF signalling pathways, and for generating a three-dimensional structure for an unknown molecule or molecular complex

SQ Sequence 112 AA;

Query Match 100.0%; Score 587; DB 5; Length 112;  
Best Local Similarity 100.0%; Pred. No. 1.1e-62;  
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAHKPQSLDTPATLYAVVENVPLRWKEFVKRLGSLDHEIDRLQLNGRCLREAYSM 60  
Db 1 MAHKPQSLDTPATLYAVVENVPLRWKEFVKRLGSLDHEIDRLQLNGRCLREAYSM 60  
QY 61 LATWRRRTPRREATLELLGRVLRDMDLGCLDEIEEALCGPAALPPAPSLLR 112  
Db 61 LATWRRRTPRREATLELLGRVLRDMDLGCLDEIEEALCGPAALPPAPSLLR 112

RESULT 2  
ABB81749  
ID ABB81749 standard; protein; 111 AA.  
XX ABB81749;  
AC ABB81749;  
DT 10-SEP-2002 (first entry)  
XX Tumour necrosis factor receptor 1 death domain (shorter sequence).  
DE Tumour necrosis factor receptor 1; receptor; TNFR-1; death domain;  
KW receptor signalling; TNFR-1 DD; protein co-ordinate data.  
XX Unidentified.  
OS  
FH  
XX Key Location/Qualifiers  
FT Region 15..21  
FT /label= Alpha\_helix\_1  
FT Region 28..34  
FT /label= Alpha\_helix\_2  
FT Region 38..42  
FT /label= Alpha\_helix\_3  
FT Region 52..65  
FT /label= Alpha\_helix\_4  
FT Region 72..85  
FT /label= Alpha\_helix\_5  
FT Region 89..98  
FT /label= Alpha\_helix\_6  
XX US2002045578-A1.  
XX  
XX  
PD 18-APR-2002.  
XX  
XX  
PF 14-MAY-2001; 2001US-00854906.  
XX  
XX  
PR 22-MAY-2000; 2000US-0206215P.  
XX  
XX (SUKI//) SUKITS S.F.  
PA (XUGG//) XU G.  
PA (LINL//) LIN L.  
PA (TELL//) TELLIEZ J.  
PA (HSUS//) HSU S.  
XX  
XX  
PI Sukits SF, Xu G, Lin L, Telliez J, Hsu S;  
XX WPI; 2002-443412/47.  
XX  
XX Solution comprising tumor necrosis factor receptor 1 death domain, useful  
PT for identifying potential inhibitor of tumor necrosis factor receptor 1  
PT death domain.  
XX  
XX Claim 1; Fig 4; 49pp; English.  
XX  
XX The sequence represents the tumour necrosis factor receptor 1 death  
CC domain (TNFR-1 DD), which is the intracellular functional domain  
CC responsible for the receptor signalling activities. The invention relates  
CC to a novel solution comprising a tumour necrosis factor receptor 1 death  
CC domain. The solution is useful for identifying a potential inhibitor of

CC TNFR-1 DD, for the design and selection of potent and selective  
CC inhibitors of TNF signalling pathways, and for generating a three-  
CC dimensional structure for an unknown molecule or molecular complex  
XX  
SQ Sequence 111 AA;  
Query Match 98.6%; Score 579; DB 5; Length 111;  
Best Local Similarity 99.1%; Pred. No. 9.9e-62;  
Matches 110; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 AHKPQSLDTPATLYAVVENVPLRWKEFVKRLGSLDHEIDRLQLNGRCLREAYSM 61  
Db 1 AHKPQSLDTPATLYAVVENVPLRWKEFVKRLGSLDHEIDRLQLNGRCLREAYSM 60  
QY 62 ATWRRRTPRREATLELLGRVLRDMDLGCLDEIEEALCGPAALPPAPSLLR 112  
Db 61 ATWRRRTPRREATLELLGRVLRDMDLGCLDEIEEALCGPAALPPAPSLLR 111

RESULT 3  
ABG70127  
ID ABG70127 standard; protein; 158 AA.  
XX  
AC ABG70127;  
XX  
DT 21-OCT-2002 (first entry)  
XX  
DE Human prey protein for Shigella ipaD #4.  
XX  
KW Prey protein; ospB; ospD1; ipaD; ipaC; ipaH9.8; ospG; ospC1; Shigella;  
KW shigellosis; bacillary dysentery; antibacterial; yeast two-hybrid system;  
XX protein-protein interaction; SID; selected interacting domain; human.  
OS Homo sapiens.  
XX WO200257303-A2.  
XX  
PD 25-JUL-2002.  
XX  
PF 11-JAN-2002; 2002WO-EP000777.  
XX  
PR 12-JAN-2001; 2001US-0261130P.  
XX  
PA (HYBR-) HYBRIGENICS.  
XX  
PI Legrain P;  
XX  
XX WPI; 2002-599706/64.  
DR N-PSDB; ABS51520.  
XX  
PT New complex of protein-protein interactions between a bait Shigella  
PT flexneri polypeptide and a prey mammalian or human placenta polypeptide  
PT for treating or preventing bacillary dysentery in a mammal or human.  
XX  
PS Claim 7; Page 94; 162pp; English.  
XX  
XX The invention relates to a complex of protein-protein interactions  
CC between a Shigella flexneri polypeptide (e.g. ospB, ospD1, ipaD, ipaC,  
CC ipaH9.8, ospG and ospC1) and a mammalian polypeptide defined in the  
CC specification. The complexes are formed using the yeast two-hybrid  
CC system. Also included are (1) a recombinant host cell expressing the  
CC interactions between the Shigella flexneri polypeptide and a mammalian  
CC polypeptide defined in the specification; (2) selecting a modulating  
CC compound that inhibits or activates the protein-protein interactions; (3)  
CC a modulating compound obtained from the method of (2); (4) a SID  
CC (selected interacting domain) polypeptide or its fragment or variant  
CC comprising the human polypeptides appearing as ABG70042-ABG70242; (5) a  
CC SID polynucleotide or its fragment or variant comprising encoding the  
CC above polypeptides a vector comprising (5); (6) a recombinant host cell  
CC containing the vector; and (10) a protein chip comprising Shigella  
CC flexneri polypeptide and a mammalian polypeptide defined in the  
CC specification. A pharmaceutical composition comprising the compound,  
CC polypeptide or polynucleotide is useful for treating or preventing



CC shigellosis (bacillary dysentery) in a human or mammal. The present  
CC sequence represents a human prey protein isolated by the yeast two-hybrid  
CC assay, forming a complex of the invention with a shigella protein  
XX  
SQ Sequence 158 AA;

Query Match 98.6%; Score 579; DB 5; Length 158;  
Best Local Similarity 99.1%; Pred. No. 1.5e-61;  
Matches 110; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 AHKPSLDTDDPATLYAVVENVPLRWKEFVKRLGLSDHEIDRLQLNGRCLREAQYSML 61  
Db |||||  
48 AHKPSLDTDDPATLYAVVENVPLRWKEFVKRLGLSDHEIDRLQLNGRCLREAQYSML 107  
|||

QY 62 ATWRRTPRREATLELLGRVLRDMDLLGCLDIEEALCGPAALPPAPSLLR 112  
Db |||||  
108 ATWRRTPRREATLELLGRVLRDMDLLGCLDIEEALCGPAALPPAPSLLR 158  
|||

RESULT 4  
ABW00828  
ID ABW00828 standard; protein; 426 AA.

AC ABW00828;

DT 15-JAN-2004 (first entry)

DE Human p55-R protein.

XX Intracellular domain; IC; p55 tumour necrotic factor receptor; TNF;  
KW tumour; rheumatoid arthritis; inflammatory disease; gene therapy;  
KW cytosstatic; human.

XX Homo sapiens.

FX Key Location/Qualifiers

FT Domain 206..426

FT /note= "p55 intracellular domain (IC)"

FT Domain 328..426

FT /note= "Death domain"

XX US6579697-B1.

PN 17-JUN-2003.

XX 12-NOV-1996; 96US-00747562.

XX 11-MAY-1995; 95WO-US005854.

XX (YEDA ) YEDA RES & DEV CO LTD.

XX Wallach D, Boldin M, Mett I, Varfolomeev E;

XX WPI; 2003-799831/75.

XX New DNA molecule encoding a polypeptide capable of binding to an  
PT intracellular domain of a p55 tumor necrotic factor (TNF) receptor,  
PT useful for preparing a composition for treating tumor, rheumatoid  
PT arthritis or inflammatory diseases.

XX Claim 1; Col 101-104; 126pp; English.

XX The invention relates to an isolated DNA molecule which encodes a  
CC polypeptide capable of binding to an intracellular domain of a p55 tumour  
CC necrotic factor (TNF) receptor. The DNA molecule is useful for preparing  
CC a composition for treating tumour, rheumatoid arthritis or inflammatory  
CC diseases. The invention is useful in gene therapy. The present sequence  
CC is the human p55IC-R protein

XX Sequence 426 AA;

Query Match 98.6%; Score 579; DB 7; Length 426;  
Best Local Similarity 99.1%; Pred. No. 5.4e-61;

Matches 110; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 AHKPSLDTDDPATLYAVVENVPLRWKEFVKRLGLSDHEIDRLQLNGRCLREAQYSML 61  
Db |||||

316 AHKPSLDTDDPATLYAVVENVPLRWKEFVKRLGLSDHEIDRLQLNGRCLREAQYSML 375  
|||

QY 62 ATWRRTPRREATLELLGRVLRDMDLLGCLDIEEALCGPAALPPAPSLLR 112  
Db |||||

376 ATWRRTPRREATLELLGRVLRDMDLLGCLDIEEALCGPAALPPAPSLLR 426  
|||

RESULT 5

AAB50895  
ID AAB50895 standard; protein; 453 AA.

XX AAB50895;

XX 19-MAR-2001 (first entry)

XX Human TNFR 1.

XX Human; TR10 receptor; cytostatic; immunosuppressive; neuroprotective;  
KW antiinflammatory; anti-HIV; antiparkinsonian; nootropic; cardiant;  
KW vasotropic; antiallergic; antidiabetic; vulnerary; ophthalmological;  
KW antiviral; antibacterial; antifungal; antiparasitic; gene therapy; TNFR;  
KW tumour necrosis factor receptor; cancer; leukaemia; autoimmune disorder;  
KW apoptosis; cardiovascular disorder; inflammatory disease; wound;  
KW infection; neurological disease; protein coordinate data.

XX Homo sapiens.

XX WO200073321-A1.

XX 07-DEC-2000.

XX 26-MAY-2000; 2000WO-US014554.

XX 28-MAY-1999; 99US-0136786P.

XX 07-JUL-1999; 99US-0142563P.

XX 15-JUL-1999; 99US-0144023P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Ni J;

XX WPI; 2001-025250/03.

XX Nucleic acid encoding a tumor necrosis factor receptor 10, useful in the  
PT diagnosis, treatment or prevention of cancer, autoimmune disorders, and  
PT diseases and disorders associated with apoptosis.

XX Disclosure; Fig 2; 212pp; English.

XX The present sequence is given in a specification relating to an isolated  
CC nucleic acid encoding a human tumour necrosis factor receptor TR10. The  
CC TR10 polynucleotide, polypeptide, antibodies, agonists and antagonists  
CC are useful in the diagnosis, treatment or prevention of cancer, such as  
CC breast and ovarian cancer and leukaemia; autoimmune disorders such as  
CC multiple sclerosis, Crohn's disease and graft versus host disease;  
CC diseases associated with increased apoptosis such as AIDS, Alzheimer's  
CC disease and Parkinson's disease; cardiovascular disorders such as limb  
CC ischaemia and congenital heart defects; inflammatory diseases e.g.  
CC allergy; wound healing; disorders associated with neovascularisation,  
CC e.g. diabetic retinopathy; infectious diseases such as viral, bacterial,  
CC fungal and parasitic infections; and neurological diseases such as  
CC amyotrophic lateral sclerosis

XX Sequence 453 AA;

Query Match 98.6%; Score 579; DB 4; Length 453;  
Best Local Similarity 99.1%; Pred. No. 5.8e-61;

Matches 110; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 AHKPSLDTDDPATLYAVVENVPLRWKEFVKRLGLSDHEIDRLQNGRCLREAYSM 61  
Db 343 AHKPSLDTDDPATLYAVVENVPLRWKEFVKRLGLSDHEIDRLQNGRCLREAYSM 402  
QY 62 ATWRRTPRREATLELLGRVLRMDLLGCLDIEEALCGPAALPPAPSLR 112  
Db 403 ATWRRTPRREATLELLGRVLRMDLLGCLDIEEALCGPAALPPAPSLR 453

RESULT 6  
ABG74755  
ID ABG74755 standard; protein; 455 AA.  
XX  
AC ABG74755;  
XX  
DT 14-MAY-2003 (first entry)  
XX  
DE Human TNF-R protein huTNF-R.  
XX  
KW TNF; human; tumour necrosis factor; tumour necrosis factor receptor;  
KW TNF-R; tumour necrosis factor binding protein; TNF-BP; tumour.  
XX  
OS Homo sapiens.  
XX  
PN EP393438-A.  
XX  
PD 24-OCT-1990.  
XX  
PF 06-APR-1990; 90EP-00106624.  
XX  
PR 21-APR-1989; 89DE-03913101.  
PR 21-JUN-1989; 89DE-03920282.  
XX  
PA (BOEH ) BOEHRINGER INGELHEIM INT GMBH.  
PA (SYND ) SYNERGEN INC.  
XX  
PI Hauptmann R, Himmler A, Maurerfogy I, Stratowa C;  
XX  
DR WPI; 1990-321987/43.  
DR N-PSDB; ABQ77487.  
XX  
PT DNA encoding TNF binding protein and TNF- receptor - used in tumour  
PT treatment and to understand mechanisms to TNF action.  
XX  
PS Example 9; Fig 9; 51pp; German.  
XX  
CC This invention describes novel polynucleotide sequences encoding tumour  
CC necrosis factor (TNF) receptor (TNF-R) or TNF binding protein (TNF-BP).  
CC The products of the invention are useful in pharmaceutical compositions  
CC for prophylaxis or treatment of human tumours and to understand the  
CC mechanisms of TNF action. This sequence represents the huma TNF-R, huTNF-  
CC R described in the disclosure of the invention  
XX  
SQ Sequence 455 AA;

Query Match 98.6%; Score 579; DB 2; Length 455;  
Best Local Similarity 99.1%; Pred. No. 5.9e-61;  
Matches 110; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 AHKPSLDTDDPATLYAVVENVPLRWKEFVKRLGLSDHEIDRLQNGRCLREAYSM 61  
Db 345 AHKPSLDTDDPATLYAVVENVPLRWKEFVKRLGLSDHEIDRLQNGRCLREAYSM 61  
QY 62 ATWRRTPRREATLELLGRVLRMDLLGCLDIEEALCGPAALPPAPSLR 112  
Db 405 ATWRRTPRREATLELLGRVLRMDLLGCLDIEEALCGPAALPPAPSLR 455

RESULT 7  
AAR07451  
ID AAR07451 standard; protein; 455 AA.  
XX  
AC AAR07451;

XX 25-MAR-2003 (revised)  
DT 29-JAN-1991 (first entry)  
XX  
DE Human Tumour Necrosis Factor-Receptor from lambdaTNF-R2 cDNA insert.  
XX  
KW Tumour necrosis factor binding protein; TNF-BP; TNF-receptor;  
KW infectious disease; parasitic disease; cachexia; autoimmune disease;  
KW shock; lambdaTNF-R2; raTNF-R8.  
XX  
OS Homo sapiens.  
XX  
PN EP393438-A.  
XX  
PD 24-OCT-1990.  
XX  
PF 06-APR-1990; 90EP-00106624.  
XX  
PR 21-APR-1989; 89DE-03913101.  
PR 21-JUN-1989; 89DE-03920282.  
XX  
PA (BOEH ) BOEHRINGER INGELHEIM INT GMBH.  
PA (SYND ) SYNERGEN INC.  
XX  
PI Hauptmann R, Himmler A, Maurerfogy I, Stratowa C;  
XX  
DR WPI; 1990-321987/43.  
DR N-PSDB; AAQ06285.  
XX  
PT DNA encoding TNF binding protein and TNF- receptor - used in tumour  
PT treatment and to understand mechanisms to TNF action.  
XX  
PS Disclosure; Fig 91(1-2); 51pp; German.  
XX  
CC raTNF-R8 (AAQ06284) was used to screen the HS913T cDNA library. LambdaTNF  
CC -R2 encodes the complete human TNF-R2 and was used to construct a plasmid  
CC (pADTNF-R) expressing the product the same way as pADTNF-BP (see  
CC AAQ06282). The expressed proteins are useful prophylactically and  
CC therapeutically to control disorders which involve the damaging effects  
CC of TNF-alpha or -beta (e.g. infectious or parasitic diseases, shock,  
CC cachexia, autoimmune diseases, adult respiratory distress syndrome etc.,  
CC or side effects of treatment with TNG-alpha). They can also be used as  
CC diagnostic reagents for assaying TNF and in study of TNF-receptor  
CC interactions. See also AAQ06282-Q06285. (Updated on 25-MAR-2003 to  
CC correct PA field.) (Updated on 25-MAR-2003 to correct PI field.)  
XX  
SQ Sequence 455 AA;

Query Match 98.6%; Score 579; DB 2; Length 455;  
Best Local Similarity 99.1%; Pred. No. 5.9e-61;  
Matches 110; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 AHKPSLDTDDPATLYAVVENVPLRWKEFVKRLGLSDHEIDRLQNGRCLREAYSM 61  
Db 345 AHKPSLDTDDPATLYAVVENVPLRWKEFVKRLGLSDHEIDRLQNGRCLREAYSM 404  
QY 62 ATWRRTPRREATLELLGRVLRMDLLGCLDIEEALCGPAALPPAPSLR 112  
Db 405 ATWRRTPRREATLELLGRVLRMDLLGCLDIEEALCGPAALPPAPSLR 455

RESULT 8  
ABG74751  
ID ABG74751 standard; protein; 455 AA.  
XX  
AC ABG74751;  
XX  
DT 14-MAY-2003 (first entry)  
XX  
DE Human TNF receptor protein.  
XX  
KW TNF; human; tumour necrosis factor; tumour necrosis factor receptor;  
KW TNF-R; tumour necrosis factor binding protein; TNF-BP; tumour.

XX Homo sapiens.  
XX OS  
XX EP393438-A.  
XX PN  
XX 24-OCT-1990.  
XX PD  
XX 06-APR-1990; 90EP-00106624.  
XX PF  
XX 21-APR-1989; 89DE-03913101.  
XX PR  
XX 21-JUN-1989; 89DE-03920282.  
XX PR  
XX (BOEH ) BOEHRINGER INGELHEIM INT GMBH.  
XX PA  
XX (SYND ) SYNERGEN INC.  
XX PA  
XX Hauptmann R, Himmler A, Maurerfogy I, Stratowa C;  
XX PI  
XX WPI; 1990-321987/43.  
XX DR  
XX DNA encoding TNF binding protein and TNF- receptor - used in tumour  
XX PT treatment and to understand mechanisms to TNF action.  
XX FT  
XX Claim 22; Page 34; 5lpp; German.  
XX PS  
XX This invention describes novel polynucleotide sequences encoding tumour  
XX CC necrosis factor (TNF) receptor (TNF-R) or TNF binding protein (TNF-BP).  
XX CC The products of the invention are useful in pharmaceutical compositions  
XX CC for prophylaxis or treatment of human tumours and to understand the  
XX CC mechanisms of TNF action. This sequence represents the TNF receptor  
XX CC described in the disclosure of the invention  
XX PA  
XX Sequence 455 AA;  
SQ  
Query Match 98.6%; Score 579; DB 2; Length 455;  
Best Local Similarity 99.1%; Pred. No. 5.9e-61;  
Matches 110; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 2 AHKPQSLDTDDPATLYAVVENVPPLRWKEFVKRLGLSDHEIDRLQLNGRCLREAQYSML 61  
Db 345 AHKPQSLDTDDPATLYAVVENVPPLRWKEFVKRLGLSDHEIDRLQLNGRCLREAQYSML 404  
QY 62 ATWRRRTPRREATLELLGRVLRDMDLLGCLDIEEALCGPAALPPAPSLLR 112  
Db 405 ATWRRRTPRREATLELLGRVLRDMDLLGCLDIEEALCGPAALPPAPSLLR 455  
RESULT 9  
AAR12550  
ID AAR12550 standard; protein; 455 AA.  
XX AC AAR12550;  
XX 25-MAR-2003 (revised)  
DT 12-SEP-1991 (first entry)  
XX Type I TNF receptor.  
DE Tumour Necrosis Factor; TNF; binding protein; TBP-I.  
XX Homo sapiens.  
OS  
XX Key Peptide Location/Qualifiers  
FT 1..21  
FT /label= sig\_peptide  
FT 21..203  
FT /label= soluble domain  
FT /note= "may be 2 amino acids shorter or contain a few  
FT additional amino acids"  
FT 22..455  
FT /label= mat\_protein  
FT 41..53  
FT /label= TBP-I derived sequence  
FT 44..83

FT Modified-site /label= repeat\_1  
FT 54..56  
FT /label= N-glycosylation\_site  
FT 84..126  
FT /label= repeat\_2  
FT 110..124  
FT /label= TBP-I derived sequence  
FT 127..167  
FT /label= repeat\_3  
FT 145..147  
FT /label= N-glycosylation\_site  
FT 151..153  
FT /label= N-glycosylation\_site  
FT 168..201  
FT /label= repeat\_4  
FT 199..201  
FT /label= TBP-I derived sequence  
FT 212..234  
FT /label= transmembrane\_domain  
XX EP433900-A.  
PN 26-JUN-1991.  
XX  
XX 13-DEC-1990; 90EP-00124133.  
XX PF  
XX 13-DEC-1989; 89IL-00092697.  
XX PR  
XX 12-JUL-1990; 90IL-00095064.  
XX PR  
XX (YEDA ) YEDA RES & DEV CO LTD.  
XX PA (WALL/) WALLACH D.  
XX PA  
XX Wallach D, Nophar Y, Kemper O, Engelmann H, Brakebusch C;  
PI Aderka D;  
XX WPI; 1991-186774/26.  
XX N-PSDB; AAQ12215.  
DR  
XX Recombinant tumour necrosis factor binding protein I - prepd. by  
PT transfecting eukaryotic cells with vector contg. deoxyribonucleic acid  
PT encoding human type I TNF receptor or soluble domain.  
XX  
XX Disclosure; Fig 1(D); 30pp; English.  
XX The Tumour Necrosis Factor Binding Protein I is the soluble form of type  
CC I TNF-receptor and constitutes a fragment of the cell surface form of  
CC this receptor, corresp. to its extracellular domain. The soluble proteins  
CC produced by the transfected cells secreted into the medium may have at  
CC the N-terminus the sequence Asp-Ser-Val (41-43), or the sequence Leu-Val-  
CC Pro (30-32) or Ile-Tyr-Pro (22-24) or any other sequence between Ile (21)  
CC and Asp (41). See also AAQ12212-15. (Updated on 25-MAR-2003 to correct PA  
CC field.)  
XX  
XX Sequence 455 AA;  
SQ  
Query Match 98.6%; Score 579; DB 2; Length 455;  
Best Local Similarity 99.1%; Pred. No. 5.9e-61;  
Matches 110; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 2 AHKPQSLDTDDPATLYAVVENVPPLRWKEFVKRLGLSDHEIDRLQLNGRCLREAQYSML 61  
Db 345 AHKPQSLDTDDPATLYAVVENVPPLRWKEFVKRLGLSDHEIDRLQLNGRCLREAQYSML 404  
QY 62 ATWRRRTPRREATLELLGRVLRDMDLLGCLDIEEALCGPAALPPAPSLLR 112  
Db 405 ATWRRRTPRREATLELLGRVLRDMDLLGCLDIEEALCGPAALPPAPSLLR 455  
RESULT 10  
AAR10986  
ID AAR10986 standard; protein; 455 AA.  
XX  
XX AAR10986;

XX 25-MAR-2003 (revised)  
DT 13-MAY-1991 (first entry)  
XX  
DE 30kD TNF inhibitor precursor.  
XX  
KW Tumour necrosis factor; inhibitor.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Cleavage-site 40..41  
FT /note= " cleavage gives active protein "  
XX  
PN AU9058976-A.  
XX  
XX 24-JAN-1991.  
PD  
XX  
PF 16-JUL-1990; 90AU-00058976.  
XX  
PR 18-JUL-1989; 89US-00381080.  
PR 11-DEC-1989; 89US-00450329.  
PR 07-FEB-1990; 90US-00479661.  
XX  
PA (SYND ) SYNERGEN INC.  
XX  
XX WPI; 1991-073847/11.  
DR N-PSDB; AAQ10883.  
DR  
XX Tumour necrosis factor inhibitor - for suppression of tn timer-alpha and -  
PT beta, useful as therapeutic agent.  
FT  
XX Disclosure; Fig 21; 142pp; English.  
PS  
XX The sequence comprises the entire 30 kD TNF inhibitor. The clone from  
CC which the sequence was deduced was isolated from a cDNA library prep.  
CC from RNA form U937 cells treated with PMA/PHA. The whole gene can be  
CC inserted into expression vectors for prep. of TNF inhibitor for use in  
CC the treatment of inflammatory and degenerative diseases. The active  
CC protein is claimed (Claim 8). See also AAR10984 and AAR11001. (Updated on  
CC 25-MAR-2003 to correct PA field.)  
XX  
SQ Sequence 455 AA;  
Query Match 98.6%; Score 579; DB 2; Length 455;  
Best Local Similarity 99.1%; Pred. No. 5.9e-61;  
Matches 110; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 2 AHKPSLDTDDPATLYAVVENVPLRWKEFVKRLGLSDHEIDRLQLNGRCLREAYQYSML 61  
Db 345 AHKPSLDTDDPATLYAVVENVPLRWKEFVKRLGLSDHEIDRLQLNGRCLREAYQYSML 404  
QY 62 ATWRRTPRREATLELLGRVLRDMDLLGCLDIEEALCGPAALPPAPSLLR 112  
Db 405 ATWRRTPRREATLELLGRVLRDMDLLGCLDIEEALCGPAALPPAPSLLR 455  
RESULT 11  
AAR11082  
ID AAR11082 standard; protein; 455 AA.  
XX  
AC AAR11082;  
XX  
DT 09-JAN-2003 (revised)  
DT 24-MAY-1991 (first entry)  
XX  
XX Human 55kD TNF-binding protein.  
XX  
KW Tumour Necrosis Factor; binding proteins; septic shock;  
KW autoimmune glomerulonephritis; lymphokine; cytokine.  
XX  
OS Homo sapiens.  
XX

FH Key Location/Qualifiers  
FT Peptide 1..28  
FT /label= signal peptide  
FT Modified-site 54  
FT /label= putative N-glycosylation site  
FT Modified-site 145  
FT /label= putative N-glycosylation site  
FT Modified-site 151  
FT /label= putative N-glycosylation site  
FT Region 212..230  
FT /label= transmembrane region  
FT Modified-site 270  
FT /label= putative N-glycosylation site  
XX  
PN EP417563-A.  
XX  
XX 20-MAR-1991.  
PD  
XX  
PF 31-AUG-1990; 90EP-00116707.  
XX  
PR 12-SEP-1989; 89CH-00003319.  
PR 08-MAR-1990; 90CH-00000746.  
PR 20-APR-1990; 90CH-00001347.  
XX  
PA (HOFF ) HOFFMANN-LA ROCHE AG.  
XX  
XX Brockhaus M, Dembic Z, Gentz R, Lesslauer W, Lotscher H;  
PI Schlaeger EJ;  
XX  
DR WPI; 1991-081851/12.  
DR N-PSDB; AAQ10955.  
XX  
PT Insoluble tumour necrosis factor binding proteins - and DNA encoding  
PT them, useful in pharmaceutical prods. and for antibody prodn.  
XX  
PS Claim 1; Fig 1; 26pp; German.  
XX  
CC Partial amino acid sequences were determined for the 55 and 75kD TNF-BPs  
CC (see AAR11072-R11081) and oligonucleotide primers were synthesised based  
CC on these partial sequences. The primers were used to produce a cDNA  
CC fragment for use as a probe to screen a human placental cDNA bank  
CC constructed in lambda gt11. Positive clones were identified and sequenced.  
CC DNA constructs comprising the TNF-BP coding sequence may also contain a  
CC fragment encoding a human Ig domain. Recombinant constructs are used to  
CC transform cells to confer improved TNF-binding properties. See also  
CC AAQ10956. (Updated on 09-JAN-2003 to add missing OS field.)  
XX  
SQ Sequence 455 AA;  
Query Match 98.6%; Score 579; DB 2; Length 455;  
Best Local Similarity 99.1%; Pred. No. 5.9e-61;  
Matches 110; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 2 AHKPSLDTDDPATLYAVVENVPLRWKEFVKRLGLSDHEIDRLQLNGRCLREAYQYSML 61  
Db 345 AHKPSLDTDDPATLYAVVENVPLRWKEFVKRLGLSDHEIDRLQLNGRCLREAYQYSML 404  
QY 62 ATWRRTPRREATLELLGRVLRDMDLLGCLDIEEALCGPAALPPAPSLLR 112  
Db 405 ATWRRTPRREATLELLGRVLRDMDLLGCLDIEEALCGPAALPPAPSLLR 455  
RESULT 12  
AAR20787  
ID AAR20787 standard; protein; 455 AA.  
XX  
AC AAR20787;  
XX  
DT 11-MAY-1992 (first entry)  
XX  
DE TNF-alpha binding protein.  
XX  
KW Tumour necrosis factor alpha; autoimmune diseases; cachectin;



KW extracellular domain.  
XX  
XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FT Peptide 1..40  
FT /note= "signal peptide"  
FT Domain 30..199  
FT /note= "extracellular domain"  
FT Peptide 41..455  
FT /note= "mature peptide"  
FT Modified-site 145..147  
FT /note= "potential N-glycosylation site"  
FT Modified-site 151..153  
FT /note= "potential N-glycosylation site"  
FT Domain 212..234  
FT /note= "transmembrane domain"  
XX  
XX  
PN GB2246569-A.  
XX  
XX 05-FEB-1992.  
PD  
XX  
XX 15-JUN-1990; 90GB-00013410.  
PF  
XX 15-JUN-1990; 90GB-00013410.  
PR  
XX (CHAR-) CHARING CROSS SUNLE.  
XX  
XX Feldman M, Gray P, Turner M, Brennan F;  
PI  
XX WPI; 1992-043613/06.  
DR N-PSDB; AAQ20973.  
XX  
XX New tumour necrosis factor alpha binding protein and polypeptide - useful  
PT in treating cachexia, sepsis and auto immune diseases e.g. rheumatoid  
PT arthritis.  
PT  
XX  
XX Disclosure; Fig 1; 25pp; English.  
PS  
XX The amino acid sequence is that of tumour necrosis factor alpha binding  
CC protein which contains the extracellular domain of human TNF alpha  
CC receptor. It is soluble and can be used in the regulation of TNF-mediated  
CC responses by binding and sequestering the cytokine. It can therefore be  
CC used therapeutically to treat disorders such as cachexia, sepsis and  
CC autoimmune diseases, specifically rheumatoid arthritis  
XX  
XX Sequence 455 AA;  
SQ  
Query Match 98.6%; Score 579; DB 2; Length 455;  
Best Local Similarity 99.1%; Pred. No. 5.9e-61;  
Matches 110; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 2 AHKPQSLDTPATLYAVVENVPLRWKEFVKRLGSLDHEIDRLQLONGRCLREAAQYSML 61  
Db 345 AHKPQSLDTPATLYAVVENVPLRWKEFVKRLGSLDHEIDRLQLONGRCLREAAQYSML 404  
QY 62 ATWRRTPRREATLELLGRVLRDMDLLGCLDIEEALCGPAALPPAPSLR 112  
Db 405 ATWRRTPRREATLELLGRVLRDMDLLGCLDIEEALCGPAALPPAPSLR 455  
RESULT 13  
AAR42059  
ID AAR42059 standard; protein; 455 AA.  
XX  
XX AAR42059;  
AC  
XX 27-AUG-2003 (revised)  
DT  
DT 25-MAR-2003 (revised)  
DT 29-APR-1994 (first entry)  
XX  
XX Lambda derived TNF-R.  
XX

KW Human; tumour necrosis factor receptor; TNF-R; interleukin-1 receptor;  
KW IL-1R; fusion protein; linker; TNF; IL-1; cachexia; cerebral malaria;  
KW rheumatoid arthritis; diabetes; multiple sclerosis; septic shock;  
KW pulmonary fibrosis; silicosis; allograft; xenograft; rejection;  
KW graft verses host disease; sepsis; inflammation; allergy;  
KW autoimmune dysfunction.  
XX  
XX Homo sapiens.  
OS Bacteriophage lambda.  
OS  
XX  
XX Key Location/Qualifiers  
FH Peptide 1..40  
FT /note= "Signal peptide"  
FT Protein 41..455  
FT /note= "Mature hTNF-R"  
XX  
PN WO9319777-A1.  
XX  
XX 14-OCT-1993.  
PD  
XX  
XX 26-MAR-1993; 93WO-US002938.  
PF  
XX 30-MAR-1992; 92US-00860710.  
PR  
XX (IMMV ) IMMUNEX CORP.  
PA  
XX Smith CA;  
PI  
XX WPI; 1993-336592/42.  
DR N-PSDB; AAQ49932.  
XX  
XX New fusion protein tumour necrosis factor and human interleukin-1  
PT receptor - useful in therapy, diagnosis and assays of e.g. rheumatoid  
PT arthritis, diabetes, cerebral malaria, sepsis, etc.  
XX  
XX Disclosure; Page 57-59; 85pp; English.  
PS  
XX The sequences given in AAR42058-59 represent human tumour necrosis  
CC factor receptor (TNF-R) and the sequences in AAR42060-61 represent human  
CC interleukin-1 receptor (IL-1R). These sequences were used in the  
CC production of a fusion protein which conformed to one of the formulae:  
CC TNF-R-linker-TNF-R-linker-IL-1R IL-1R-linker-TNF-R-linker-TNF-R Or TNF-R-  
CC linker-TNF-R The linker may comprise 5-100 amino acids selected from Gly,  
CC Asp, Ser, Thr and Ala. These linkers separate the individual moieties by  
CC such a distance that each component of the fusion protein is capable of  
CC folding into the secondary or tertiary structure required for its  
CC biological activity. These fusion proteins may be used in therapy,  
CC diagnosis and assays for conditions mediated by TNF or IL-1, particularly  
CC in conditions in which both TNF and IL-1 play a causative role. They may  
CC be used to treat cachexia, rheumatoid arthritis, diabetes, multiple  
CC sclerosis, pulmonary fibrosis and silicosis, cerebral malaria, allograft  
CC and xenograft rejection in graft verses host disease, sepsis, septic  
CC shock, inflammation, allergies and autoimmune dysfunctions. (Updated on  
CC 25-MAR-2003 to correct PN field.) (Updated on 27-AUG-2003 to correct OS  
CC field.)  
XX  
SQ Sequence 455 AA;  
Query Match 98.6%; Score 579; DB 2; Length 455;  
Best Local Similarity 99.1%; Pred. No. 5.9e-61;  
Matches 110; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 2 AHKPQSLDTPATLYAVVENVPLRWKEFVKRLGSLDHEIDRLQLONGRCLREAAQYSML 61  
Db 345 AHKPQSLDTPATLYAVVENVPLRWKEFVKRLGSLDHEIDRLQLONGRCLREAAQYSML 404  
QY 62 ATWRRTPRREATLELLGRVLRDMDLLGCLDIEEALCGPAALPPAPSLR 112  
Db 405 ATWRRTPRREATLELLGRVLRDMDLLGCLDIEEALCGPAALPPAPSLR 455  
RESULT 14  
AAR51034

ID XX AAR51034 standard; protein; 455 AA.  
AC AAR51034;  
DT 25-MAR-2003 (revised)  
DT 13-MAY-1994 (first entry)  
XX  
XX Mutant p55 tumour necrosis factor receptor.  
DE  
XX  
KW TNF; tumour necrosis factor; receptor; disease; autoimmunity;  
KW rheumatoid arthritis; graft rejection; graft vs. host; septic shock;  
KW effector protein.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Region 1. .21  
FT /label= Leader peptide.  
FT Domain 183. .205  
FT /label= Transmembrane domain.  
XX  
PN EP568925-A2.  
XX  
PD 10-NOV-1993.  
XX  
PF 29-APR-1993; 93EP-00106981.  
XX  
PR 03-MAY-1992; 92IL-00101769.  
XX  
PA (YEDA ) YEDA RES & DEV CO LTD.  
XX  
PI Wallach D, Brakebusch C;  
XX  
DR WPI; 1993-353057/45.  
DR N-PSDB; AAQ50870.  
XX  
PT Modulating activity of tumour necrosis factor receptor - using  
PT peptide(s), antibodies, etc. which interact with critical regions of  
PT receptor or effector protein, for controlling auto-immune disease, septic  
PT shock, etc.  
XX  
PS Claim 5; Fig 1; 17pp; English.  
XX  
CC Modification of the tumour necrosis factor receptor by mutation or  
CC deletion modulates signal transduction and/or cleavage effected by the  
CC receptor. This modulation of activity can also be achieved using effector  
CC proteins which interact with the TNF receptor. Molecules which interact  
CC with the TNF receptor or the effector proteins can be used to treat or  
CC prevent diseases associated with TNF activity e.g. autoimmune disease;  
CC rheumatoid arthritis; graft rejection; graft vs. host disease or septic  
CC shock. They can also be used to treat overdoses of exogenous TNF.  
CC Specific deletions include amino acid residues 405-426 from which it was  
CC discovered that amino acids 405-414, or part of them, are essential for  
CC the signalling of the human p55 TNF-R for the cytotoxic effect of TNF  
CC whereas amino acids 415-426 are not essential. Also residues 170-174, 174  
CC -179 or both i.e 170-179 were deleted. This region of amino acids, or  
CC part of, when deleted, abolished shedding of the soluble extracellular  
CC forms of the protein. This sequence corresponds to the wild type protein  
CC disclosed in AAR42197 except that alanine at position 197 has been  
CC substituted in place of serine. The substitution inhibits cleavage of the  
CC soluble form of the protein. (Updated on 25-MAR-2003 to correct PN  
CC field.)  
XX  
SQ Sequence 455 AA;

Query Match 98.6%; Score 579; DB 2; Length 455;  
Best Local Similarity 99.1%; Pred. No. 5.9e-61;  
Matches 110; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 AHKPQSLDTPATLYAVVENVPLRWKEFVKRLGLSDHEIDRLQLNGRCLREAYQSM 61  
Db 345 AHKPQSLDTPATLYAVVENVPLRWKEFVKRLGLSDHEIDRLQLNGRCLREAYQSM 404

QY 62 ATWRRRTPRREATLELLGRVLRDMDLLGCLIEDIEEALCGPAALPPAPSLR 112  
Db |||||  
405 ATWRRRTPRREATLELLGRVLRDMDLLGCLIEDIEEALCGPAALPPAPSLR 455  
RESULT 15  
AAR42197  
ID AAR42197 standard; protein; 455 AA.  
XX  
AC AAR42197;  
XX  
DT 25-MAR-2003 (revised)  
DT 13-MAY-1994 (first entry)  
XX  
DE p55 Tumour necrosis factor receptor.  
XX  
KW TNF; tumour necrosis factor; receptor; disease; autoimmunity;  
KW rheumatoid arthritis; graft rejection; graft vs. host; septic shock;  
KW effector protein.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Region 1. .21  
FT /label= Leader peptide.  
FT Domain 183. .205  
FT /label= Transmembrane domain.  
XX  
PN EP568925-A2.  
XX  
PD 10-NOV-1993.  
XX  
PF 29-APR-1993; 93EP-00106981.  
XX  
PR 03-MAY-1992; 92IL-00101769.  
XX  
PA (YEDA ) YEDA RES & DEV CO LTD.  
XX  
PI Wallach D, Brakebusch C;  
XX  
DR WPI; 1993-353057/45.  
DR N-PSDB; AAQ50870.  
XX  
PT Modulating activity of tumour necrosis factor receptor - using  
PT peptide(s), antibodies, etc. which interact with critical regions of  
PT receptor or effector protein, for controlling auto-immune disease, septic  
PT shock, etc.  
XX  
PS Claim 2; Fig 1; 17pp; English.  
XX  
CC Modification of the tumour necrosis factor receptor by mutation or  
CC deletion modulates signal transduction and/or cleavage effected by the  
CC receptor. This modulation of activity can also be achieved using effector  
CC proteins which interact with the TNF receptor. Molecules which interact  
CC with the TNF receptor or the effector proteins can be used to treat or  
CC prevent diseases associated with TNF activity e.g. autoimmune disease;  
CC rheumatoid arthritis; graft rejection; graft vs. host disease or septic  
CC shock. They can also be used to treat overdoses of exogenous TNF.  
CC Specific deletions include amino acid residues 405-426 from which it was  
CC discovered that amino acids 405-414, or part of them, are essential for  
CC the signalling of the human p55 TNF-R for the cytotoxic effect of TNF  
CC whereas amino acids 415-426 are not essential. Also residues 170-174, 174  
CC -179 or both i.e 170-179 were deleted. This region of amino acids, or  
CC part of, when deleted, abolished shedding of the soluble extracellular  
CC forms of the protein. (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 455 AA;

Query Match 98.6%; Score 579; DB 2; Length 455;  
Best Local Similarity 99.1%; Pred. No. 5.9e-61;  
Matches 110; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 AHKPQSLDTPATLYAVVENVPLRWKEFVKRLGLSDHEIDRLQLNGRCLREAYQSM 61



Db 345 AHKPQSLDTDDPATLYAVVENVPPLRWKEFVRRIGLSDEIDRLELQNGRCLEAQYSML 404  
Qy 62 ATWRRRTPRREATLELLGRVLRDMDLLGCLEDEIEEALCGPAALPPAPSLLR 112  
Db 405 ATWRRRTPRREATLELLGRVLRDMDLLGCLEDEIEEALCGPAALPPAPSLLR 455

Search completed: June 1, 2004, 14:43:52  
Job time : 50.9581 secs

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OM protein - protein search, using sw model

Run on: June 1, 2004, 14:41:22 ; Search time 14.0838 Seconds  
(without alignments)  
410.549 Million cell updates/sec

Title: US-09-854-906-1  
Perfect score: 587  
Sequence: 1 MAHKPQSLDTPATLYAVV.....DIEEALCGPAALPPAPSLLR 112

Scoring table: BLOSUM62  
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Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	579	98.6	426	4	US-08-747-562-37
2	579	98.6	453	3	US-09-086-483A-5
3	579	98.6	453	4	US-09-580-212-5
4	579	98.6	453	4	US-09-769-402-5
5	579	98.6	455	1	US-08-321-668-2
6	579	98.6	455	1	US-08-837-941-2
7	579	98.6	455	2	US-08-126-016-2
8	579	98.6	455	3	US-08-815-469-5
9	579	98.6	455	3	US-09-006-353A-3
10	579	98.6	455	4	US-09-527-236A-5
11	579	98.6	455	4	US-08-054-970-2
12	579	98.6	455	4	US-09-565-918-4
13	579	98.6	455	4	US-09-573-986-3
14	579	98.6	455	4	US-09-027-287-3
15	579	98.6	455	4	US-09-252-656B-3
16	579	98.6	455	4	US-08-406-824A-4
17	579	98.6	455	4	US-09-523-323-3
18	579	98.6	455	4	US-09-756-854-5
19	579	98.6	909	4	US-09-013-895A-4
20	579	98.6	909	4	US-09-448-868-4
21	574	97.8	455	1	US-08-050-319B-25
22	574	97.8	455	2	US-08-465-982-25
23	443	75.5	86	3	US-09-042-785A-25
24	443	75.5	108	2	US-08-580-988A-20
25	421	71.7	471	4	US-09-513-007-2
26	404	68.8	78	4	US-08-828-683A-23
27	394.5	67.2	84	4	US-09-069-827A-120

28	363	61.8	70	4	US-09-159-277A-6	Sequence 6, Appli
29	340.5	58.0	68	4	US-09-527-236A-23	Sequence 23, Appl
30	340.5	58.0	68	4	US-09-756-854-23	Sequence 23, Appl
31	326	55.5	64	4	US-08-894-626-3	Sequence 3, Appli
32	232	39.5	45	2	US-08-219-237B-11	Sequence 11, Appl
33	213	36.3	41	1	US-08-444-005-29	Sequence 29, Appl
34	189	32.2	41	1	US-08-444-005-23	Sequence 23, Appl
35	176	30.0	41	1	US-08-444-005-28	Sequence 28, Appl
36	166.5	28.4	35	1	US-08-444-005-35	Sequence 35, Appl
37	165	28.1	833	4	US-09-013-895A-5	Sequence 5, Appli
38	165	28.1	833	4	US-09-448-868-5	Sequence 5, Appli
39	164.5	28.0	417	3	US-08-815-469-4	Sequence 4, Appli
40	164.5	28.0	417	3	US-09-153-927-2	Sequence 2, Appli
41	164.5	28.0	417	4	US-09-565-918-5	Sequence 5, Appli
42	164.5	28.0	417	4	US-08-928-069-10	Sequence 10, Appl
43	164.5	28.0	417	4	US-08-828-683A-6	Sequence 6, Appli
44	164.5	28.0	428	3	US-08-815-469-2	Sequence 2, Appli
45	139	23.7	65	4	US-09-527-236A-24	Sequence 24, Appl

ALIGNMENTS

RESULT 1

US-08-747-562-37

; Sequence 37, Application US/08747562

; Patent No. 6579697

; GENERAL INFORMATION:

; APPLICANT: WALLACH, David

; APPLICANT: BOLDIN, Mark

; APPLICANT: METT, Igor

; APPLICANT: VARFOLOMEEV, Eugene

; TITLE OF INVENTION: MODULATOR OF TNF/NGF SUPERFAMILY RECEPTORS

; TITLE OF INVENTION: AND SOLUBLE OLIGOMERIC TNF/NGF SUPERFAMILY RECEPTORS

; NUMBER OF SEQUENCES: 37

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BROWDY AND NEIMARK

; STREET: 419 Seventh Street, N.W., Suite 300

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20004

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/747,562

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/05854

; FILING DATE: 11-MAY-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: IL 109,632

; FILING DATE: 11-MAY-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: IL 111,125

; FILING DATE: 02-OCT-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: BROWDY, Roger L.

; REGISTRATION NUMBER: 25,618

; REFERENCE/DOCKET NUMBER: WALLACH=15A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-628-5197

; TELEFAX: 202-737-3528

; INFORMATION FOR SEQ ID NO: 37:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 426 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; US-08-747-562-37

Query Match 98.6%; Score 579; DB 4; Length 426;  
Best Local Similarity 99.1%; Pred. No. 4.2e-62;  
Matches 110; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 AHKPSLTDTPATLYAVVENVPLRWKEFVKRLGLSDHEIDRLQNGRCLREAYSM 61  
Db 316 AHKPSLTDTPATLYAVVENVPLRWKEFVKRLGLSDHEIDRLQNGRCLREAYSM 375

QY 62 ATWRRTPREATLELLGRVLRDMDLLGCLEDEIEALCGPAALPPAPSLR 112  
Db 376 ATWRRTPREATLELLGRVLRDMDLLGCLEDEIEALCGPAALPPAPSLR 426

RESULT 2  
US-09-086-483A-5  
; Sequence 5, Application US/09086483A  
; Patent No. 6214580  
; GENERAL INFORMATION:  
; APPLICANT: NI, et al.  
; TITLE OF INVENTION: HUMAN TUMOR NECROSIS FACTOR RECEPTOR TR10  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.  
; STREET: 9410 KEY WEST AVENUE  
; CITY: ROCKVILLE  
; STATE: MD  
; COUNTRY: US  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/086,483A  
; FILING DATE: May-29-98  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/050,936  
; FILING DATE: May-30-97  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/069,112  
; FILING DATE: Dec-9-97  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROOKES, ANDERS A.  
; REGISTRATION NUMBER: 36,373  
; REFERENCE/DOCKET NUMBER: PF379  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (301) 309-8504  
; TELEFAX: (301) 309-8439  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 453 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-086-483A-5

Query Match 98.6%; Score 579; DB 3; Length 453;  
Best Local Similarity 99.1%; Pred. No. 4.6e-62;  
Matches 110; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 AHKPSLTDTPATLYAVVENVPLRWKEFVKRLGLSDHEIDRLQNGRCLREAYSM 61  
Db 343 AHKPSLTDTPATLYAVVENVPLRWKEFVKRLGLSDHEIDRLQNGRCLREAYSM 402

QY 62 ATWRRTPREATLELLGRVLRDMDLLGCLEDEIEALCGPAALPPAPSLR 112  
Db 403 ATWRRTPREATLELLGRVLRDMDLLGCLEDEIEALCGPAALPPAPSLR 453

RESULT 3  
US-09-580-212-5  
; Sequence 5, Application US/09580212  
; Patent No. 6506569  
; GENERAL INFORMATION:  
; APPLICANT: NI, Jian et al.  
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR10  
; FILE REFERENCE: PF379P1  
; CURRENT APPLICATION NUMBER: US/09/580,212  
; CURRENT FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/136,786  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/142,563  
; PRIOR FILING DATE: 1999-07-07  
; PRIOR APPLICATION NUMBER: 60/144,023  
; PRIOR FILING DATE: 1999-07-15  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 453  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-580-212-5

Query Match 98.6%; Score 579; DB 4; Length 453;  
Best Local Similarity 99.1%; Pred. No. 4.6e-62;  
Matches 110; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 AHKPSLTDTPATLYAVVENVPLRWKEFVKRLGLSDHEIDRLQNGRCLREAYSM 61  
Db 343 AHKPSLTDTPATLYAVVENVPLRWKEFVKRLGLSDHEIDRLQNGRCLREAYSM 402

QY 62 ATWRRTPREATLELLGRVLRDMDLLGCLEDEIEALCGPAALPPAPSLR 112  
Db 403 ATWRRTPREATLELLGRVLRDMDLLGCLEDEIEALCGPAALPPAPSLR 453

RESULT 4  
US-09-769-402-5  
; Sequence 5, Application US/09769402  
; Patent No. 6607726  
; GENERAL INFORMATION:  
; APPLICANT: NI, et al.  
; TITLE OF INVENTION: HUMAN TUMOR NECROSIS FACTOR RECEPTOR TR10  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.  
; STREET: 9410 KEY WEST AVENUE  
; CITY: ROCKVILLE  
; STATE: MD  
; COUNTRY: US  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/769,402  
; FILING DATE: 26-Jan-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/086,483  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: 60/069,112  
; FILING DATE: Dec-9-97  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROOKES, ANDERS A.  
; REGISTRATION NUMBER: 36,373  
; REFERENCE/DOCKET NUMBER: PF379  
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (301) 309-8504  
TELEFAX: (301) 309-8439  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 453 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
US-09-769-402-5

Query Match 98.6%; Score 579; DB 4; Length 453;  
Best Local Similarity 99.1%; Pred. No. 4.6e-62;  
Matches 110; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 2 AHKPSQSLDTPATLYAVVENVPPLRWKEFVKRLGLSDHEIDRLQLQNGRCLREAQYSML 61  
Db |||||  
QY 62 ATWRRTPREATLELLGRVLRMDLLGCLDIEEALCGPAALPPAPSLR 112  
Db |||||  
QY 403 ATWRRTPREATLELLGRVLRMDLLGCLDIEEALCGPAALPPAPSLR 453

RESULT 5  
US-08-321-668-2  
; Sequence 2, Application US/08321668  
; Patent No. 5665859  
; GENERAL INFORMATION:  
; APPLICANT: WALLACH, David  
; APPLICANT: BRAKEBUSCH, Cord  
; APPLICANT: VARFOLOMEEV, Eugene  
; APPLICANT: BATKIN, Michael  
; TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING OF  
; TITLE OF INVENTION: THE TNF RECEPTORS, THEIR PREPARATION AND THEIR USE  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/321,668  
; FILING DATE: 12-OCT-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: IL 107268  
; FILING DATE: 12-OCT-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWDY, Roger L.  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER: WALLACH=13  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; TELEX: 248633  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 455 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-321-668-2

Query Match 98.6%; Score 579; DB 1; Length 455;

Best Local Similarity 99.1%; Pred. No. 4.6e-62;  
Matches 110; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 2 AHKPSQSLDTPATLYAVVENVPPLRWKEFVKRLGLSDHEIDRLQLQNGRCLREAQYSML 61  
Db |||||  
QY 62 ATWRRTPREATLELLGRVLRMDLLGCLDIEEALCGPAALPPAPSLR 112  
Db |||||  
QY 405 ATWRRTPREATLELLGRVLRMDLLGCLDIEEALCGPAALPPAPSLR 455

RESULT 6  
US-08-837-941-2  
; Sequence 2, Application US/08837941  
; Patent No. 5766917  
; GENERAL INFORMATION:  
; APPLICANT: WALLACH, David  
; APPLICANT: BRAKEBUSCH, Cord  
; APPLICANT: VARFOLOMEEV, Eugene  
; APPLICANT: BATKIN, Michael  
; TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING OF  
; TITLE OF INVENTION: THE TNF RECEPTORS, THEIR PREPARATION AND THEIR USE  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/837,941  
; FILING DATE: 28-APR-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/321,668  
; FILING DATE: 12-OCT-1994  
; APPLICATION NUMBER: IL 107268  
; FILING DATE: 12-OCT-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWDY, Roger L.  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER: WALLACH=13  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; TELEX: 248633  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 455 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-837-941-2

Query Match 98.6%; Score 579; DB 1; Length 455;  
Best Local Similarity 99.1%; Pred. No. 4.6e-62;  
Matches 110; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 2 AHKPSQSLDTPATLYAVVENVPPLRWKEFVKRLGLSDHEIDRLQLQNGRCLREAQYSML 61  
Db |||||  
QY 345 AHKPSQSLDTPATLYAVVENVPPLRWKEFVKRLGLSDHEIDRLQLQNGRCLREAQYSML 404  
Db |||||  
QY 62 ATWRRTPREATLELLGRVLRMDLLGCLDIEEALCGPAALPPAPSLR 112  
Db |||||  
QY 405 ATWRRTPREATLELLGRVLRMDLLGCLDIEEALCGPAALPPAPSLR 455

RESULT 7  
US-08-126-016-2  
; Sequence 2, Application US/08126016  
; Patent No. 5811261  
; GENERAL INFORMATION:  
; APPLICANT: WALLACH, DAVID  
; APPLICANT: NOPHAR, YARON  
; APPLICANT: KEMPER, OLIVER  
; APPLICANT: ENGELMANN, HARTMUT  
; APPLICANT: BRAKEBUSCH, CORD  
; APPLICANT: ADERKA, DAN  
; TITLE OF INVENTION: EXPRESSION OF THE RECOMBINANT TUMOR  
; TITLE OF INVENTION: NECROSIS FACTOR BINDING PROTEIN I (TBP-I)  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Browdy and Neimark  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/126,016  
; FILING DATE: 24-SEP-1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/625668  
; FILING DATE: 13-DEC-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWDY, ROGER L  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER: WALLACH4  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; TELEX: 248633  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 455 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-126-016-2

Query Match 98.6%; Score 579; DB 2; Length 455;  
Best Local Similarity 99.1%; Pred. No. 4.6e-62;  
Matches 110; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 AHKPSLDTDDPATLYAVVENVPLRWKEFVKRLGLSDHEIDRLLELQNGRCLREAYSM 61  
Db 345 AHKPSLDTDDPATLYAVVENVPLRWKEFVKRLGLSDHEIDRLLELQNGRCLREAYSM 404

QY 62 ATWRRTPRREATLELLGRVLRMDLLGCLDIEEALCGPAALPPAPSLR 112  
Db 405 ATWRRTPRREATLELLGRVLRMDLLGCLDIEEALCGPAALPPAPSLR 455

RESULT 8  
US-08-815-469-5  
; Sequence 5, Application US/08815469  
; Patent No. 6153402  
; GENERAL INFORMATION:  
; APPLICANT: Yu, Guo-Liang  
; APPLICANT: Ni, Jian  
; APPLICANT: Dixit, Vishva  
; APPLICANT: Gentz, Reiner L.  
; APPLICANT: Dillon, Patrick J.

Query Match 98.6%; Score 579; DB 2; Length 455;  
Best Local Similarity 99.1%; Pred. No. 4.6e-62;  
Matches 110; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 AHKPSLDTDDPATLYAVVENVPLRWKEFVKRLGLSDHEIDRLLELQNGRCLREAYSM 61  
Db 345 AHKPSLDTDDPATLYAVVENVPLRWKEFVKRLGLSDHEIDRLLELQNGRCLREAYSM 404

QY 62 ATWRRTPRREATLELLGRVLRMDLLGCLDIEEALCGPAALPPAPSLR 112  
Db 405 ATWRRTPRREATLELLGRVLRMDLLGCLDIEEALCGPAALPPAPSLR 455

; TITLE OF INVENTION: Death Domain Containing Receptors  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.  
; STREET: 1100 New York Ave., NW, Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/815,469  
; FILING DATE: HEREWITH  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: No. 6153402 Yet Assigned  
; FILING DATE: 06-FEB-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/028,711  
; FILING DATE: 17-OCT-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/013,285  
; FILING DATE: 12-MAR-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Steffe, Eric K.  
; REGISTRATION NUMBER: 36,688  
; REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 455 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: not relevant  
; MOLECULE TYPE: protein  
US-08-815-469-5

Query Match 98.6%; Score 579; DB 3; Length 455;  
Best Local Similarity 99.1%; Pred. No. 4.6e-62;  
Matches 110; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 AHKPSLDTDDPATLYAVVENVPLRWKEFVKRLGLSDHEIDRLLELQNGRCLREAYSM 61  
Db 345 AHKPSLDTDDPATLYAVVENVPLRWKEFVKRLGLSDHEIDRLLELQNGRCLREAYSM 404

QY 62 ATWRRTPRREATLELLGRVLRMDLLGCLDIEEALCGPAALPPAPSLR 112  
Db 405 ATWRRTPRREATLELLGRVLRMDLLGCLDIEEALCGPAALPPAPSLR 455

RESULT 9  
US-09-006-353A-3  
; Sequence 3, Application US/09006353A  
; Patent No. 6261801  
; GENERAL INFORMATION:  
; APPLICANT: WEI, YING-FEI  
; APPLICANT: YU, GUO-LIANG  
; APPLICANT: GENTZ, REINER  
; APPLICANT: RUBEN, STEVEN  
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR RECEPTOR 5  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.  
; STREET: 9410 KEY WEST AVENUE  
; CITY: ROCKVILLE  
; STATE: MD  
; COUNTRY: US

Query Match 98.6%; Score 579; DB 3; Length 455;  
Best Local Similarity 99.1%; Pred. No. 4.6e-62;  
Matches 110; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 AHKPSLDTDDPATLYAVVENVPLRWKEFVKRLGLSDHEIDRLLELQNGRCLREAYSM 61  
Db 345 AHKPSLDTDDPATLYAVVENVPLRWKEFVKRLGLSDHEIDRLLELQNGRCLREAYSM 404

QY 62 ATWRRTPRREATLELLGRVLRMDLLGCLDIEEALCGPAALPPAPSLR 112  
Db 405 ATWRRTPRREATLELLGRVLRMDLLGCLDIEEALCGPAALPPAPSLR 455



; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/006,353A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BROOKES, ANDERS A
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF341
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 455 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-006-353A-3

Query Match 98.6%; Score 579; DB 3; Length 455;
Best Local Similarity 99.1%; Pred. No. 4.6e-62;
Matches 110; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 AHKPSLDTDDPATLYAVVENVPLRWKEFVKRLGLSDHEIDRLQLNGRCLREAYSM 61
Db 345 AHKPSLDTDDPATLYAVVENVPLRWKEFVKRLGLSDHEIDRLQLNGRCLREAYSM 404
QY 62 ATWRRTPREATLELLGRVLRDMDLLGCLDIEEALCGPAALPPAPSLR 112
Db 405 ATWRRTPREATLELLGRVLRDMDLLGCLDIEEALCGPAALPPAPSLR 455

RESULT 10
US-09-527-236A-5
; Sequence 5, Application US/09527236A
; Patent No. 6358508
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Fan, Ping
; APPLICANT: Gentz, Reiner L.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
; FILE REFERENCE: PF375P1
; CURRENT APPLICATION NUMBER: US/09/527,236A
; CURRENT FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/052,991
; PRIOR FILING DATE: 1997-06-11
; PRIOR APPLICATION NUMBER: 09/095,094
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/126,019
; PRIOR FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: 60/134,220
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-527-236A-5

Query Match 98.6%; Score 579; DB 4; Length 455;
Best Local Similarity 99.1%; Pred. No. 4.6e-62;
Matches 110; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 AHKPSLDTDDPATLYAVVENVPLRWKEFVKRLGLSDHEIDRLQLNGRCLREAYSM 61

Db 345 AHKPSLDTDDPATLYAVVENVPLRWKEFVKRLGLSDHEIDRLQLNGRCLREAYSM 404
QY 62 ATWRRTPREATLELLGRVLRDMDLLGCLDIEEALCGPAALPPAPSLR 112
Db 405 ATWRRTPREATLELLGRVLRDMDLLGCLDIEEALCGPAALPPAPSLR 455

RESULT 11
US-08-054-970-2
; Sequence 2, Application US/08054970
; Patent No. 6395267
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; APPLICANT: BRAKEBUSCH, Cord
; TITLE OF INVENTION: TNF RECEPTOR ACTION MODULATION
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/054,970
; FILING DATE: 03-MAY-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Townsend, Kevin G.
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: WALLACH=9
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 455 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-054-970-2

Query Match 98.6%; Score 579; DB 4; Length 455;
Best Local Similarity 99.1%; Pred. No. 4.6e-62;
Matches 110; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 AHKPSLDTDDPATLYAVVENVPLRWKEFVKRLGLSDHEIDRLQLNGRCLREAYSM 61
Db 345 AHKPSLDTDDPATLYAVVENVPLRWKEFVKRLGLSDHEIDRLQLNGRCLREAYSM 404
QY 62 ATWRRTPREATLELLGRVLRDMDLLGCLDIEEALCGPAALPPAPSLR 112
Db 405 ATWRRTPREATLELLGRVLRDMDLLGCLDIEEALCGPAALPPAPSLR 455

RESULT 12
US-09-565-918-4
; Sequence 4, Application US/09565918
; Patent No. 6433147
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A.
; APPLICANT: Pan, James G.
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Dixit, Vishva M.
; TITLE OF INVENTION: Death Domain Containing Receptor 4



FILE REFERENCE: 1488.1300005  
CURRENT APPLICATION NUMBER: US/09/565,918  
CURRENT FILING DATE: 2000-05-05  
PRIOR APPLICATION NUMBER: US 60/132,922  
PRIOR FILING DATE: 1999-05-06  
PRIOR APPLICATION NUMBER: US 09/013,895  
PRIOR FILING DATE: 1998-01-27  
PRIOR APPLICATION NUMBER: US 60/037,829  
PRIOR FILING DATE: 1997-02-05  
PRIOR APPLICATION NUMBER: US 60/035,722  
PRIOR FILING DATE: 1997-01-28  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 4  
LENGTH: 455  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-565-918-4

Query Match 98.6%; Score 579; DB 4; Length 455;  
Best Local Similarity 99.1%; Pred. No. 4.6e-62;  
Matches 110; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 2 AHKPQSLDTPATLYAVVENVPPLRWKEFVKRLGLSDHEIDRLQNGRCLREAQYSML 61  
Db 345 AHKPQSLDTPATLYAVVENVPPLRWKEFVKRLGLSDHEIDRLQNGRCLREAQYSML 404  
QY 62 ATWRRTPRREATLELLGRVLRDMDLLGCLEDEIEEALCGPAALPPAPSLR 112  
Db 405 ATWRRTPRREATLELLGRVLRDMDLLGCLEDEIEEALCGPAALPPAPSLR 455

RESULT 13  
US-09-573-986-3  
Sequence 3, Application US/09573986  
Patent No. 6455040  
GENERAL INFORMATION:  
APPLICANT: Wei, Ying-Fei  
APPLICANT: Ni, Jian  
APPLICANT: Gentz, Reiner  
APPLICANT: Ruben, Steven  
TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5  
FILE REFERENCE: 1488.1280004  
CURRENT APPLICATION NUMBER: US/09/573,986  
CURRENT FILING DATE: 2000-05-18  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 3  
LENGTH: 455  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-573-986-3

Query Match 98.6%; Score 579; DB 4; Length 455;  
Best Local Similarity 99.1%; Pred. No. 4.6e-62;  
Matches 110; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
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Db 345 AHKPQSLDTPATLYAVVENVPPLRWKEFVKRLGLSDHEIDRLQNGRCLREAQYSML 404  
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Db 405 ATWRRTPRREATLELLGRVLRDMDLLGCLEDEIEEALCGPAALPPAPSLR 455

RESULT 14  
US-09-027-287-3  
Sequence 3, Application US/09027287A  
Patent No. 6479254  
GENERAL INFORMATION:  
APPLICANT: Ebner, Reinhard  
APPLICANT: Yu, Guo-Liang

APPLICANT: Ruben, Steven M.  
APPLICANT: Ullrich, Stephen  
TITLE OF INVENTION: Apoptosis Inducing Molecule II  
FILE REFERENCE: 1488.0650004  
CURRENT APPLICATION NUMBER: US/09/027,287A  
CURRENT FILING DATE: 1998-02-20  
EARLIER APPLICATION NUMBER: US 09/003,886  
EARLIER FILING DATE: 1998-01-07  
EARLIER APPLICATION NUMBER: US 08/822,953  
EARLIER FILING DATE: 1997-03-21  
EARLIER APPLICATION NUMBER: US 60/030,157  
EARLIER FILING DATE: 1996-10-31  
EARLIER APPLICATION NUMBER: US 60/013,923  
EARLIER FILING DATE: 1996-03-22  
NUMBER OF SEQ ID NOS: 55  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 3  
LENGTH: 455  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-027-287-3

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Best Local Similarity 99.1%; Pred. No. 4.6e-62;  
Matches 110; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
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Db 345 AHKPQSLDTPATLYAVVENVPPLRWKEFVKRLGLSDHEIDRLQNGRCLREAQYSML 404  
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Db 405 ATWRRTPRREATLELLGRVLRDMDLLGCLEDEIEEALCGPAALPPAPSLR 455

RESULT 15  
US-09-252-656B-3  
Sequence 3, Application US/09252656B  
Patent No. 6495520  
GENERAL INFORMATION:  
APPLICANT: Ebner, Reinhard  
APPLICANT: Yu, Guo-Liang  
APPLICANT: Ruben, Steven M.  
APPLICANT: Zhang, Jun  
APPLICANT: Ullrich, Stephen  
APPLICANT: Zhai, Yifan  
TITLE OF INVENTION: Apoptosis Inducing Molecule II and Methods of Use  
FILE REFERENCE: 1488.0650006  
CURRENT APPLICATION NUMBER: US/09/252,656B  
CURRENT FILING DATE: 1999-02-19  
PRIOR APPLICATION NUMBER: US 60/075,409  
PRIOR FILING DATE: 1998-02-20  
PRIOR APPLICATION NUMBER: US 09/027,287  
PRIOR FILING DATE: 1998-02-20  
PRIOR APPLICATION NUMBER: US 09/003,886  
PRIOR FILING DATE: 1998-01-07  
PRIOR APPLICATION NUMBER: US 08/822,953  
PRIOR FILING DATE: 1997-03-21  
PRIOR APPLICATION NUMBER: US 60/013,923  
PRIOR FILING DATE: 1996-03-22  
PRIOR APPLICATION NUMBER: US 60/030,157  
PRIOR FILING DATE: 1996-10-31  
NUMBER OF SEQ ID NOS: 61  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 3  
LENGTH: 455  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-252-656B-3

Query Match 98.6%; Score 579; DB 4; Length 455;  
Best Local Similarity 99.1%; Pred. No. 4.6e-62;  
Matches 110; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy	62	ATWRRTPRREATLELLGRVLRDMDLLGCLEDEIEEALCGPAALPPAPSLLR	112
Db	405	ATWRRTPRREATLELLGRVLRDMDLLGCLEDEIEEALCGPAALPPAPSLLR	455

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Job time : 15.0838 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 1, 2004, 14:43:57 ; Search time 36.2156 Seconds  
(without alignments)  
863.605 Million cell updates/sec

Title: US-09-854-906-1  
Perfect score: 587  
Sequence: 1 MAHKPQSLDTPATLYAVV.....DIEALCGPAALPPAPSLR 112

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 1151071

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	579	98.6	426	15	US-10-349-977-37
3	579	98.6	453	14	US-10-280-047-5
4	579	98.6	455	9	US-09-826-212-3
5	579	98.6	455	9	US-09-333-966-5
6	579	98.6	455	9	US-09-027-287-3
7	579	98.6	455	9	US-09-874-138-3
8	579	98.6	455	9	US-09-840-707A-16
9	579	98.6	455	9	US-09-252-656B-3
10	579	98.6	455	9	US-09-899-422-2
11	579	98.6	455	9	US-09-899-422-17
12	579	98.6	455	9	US-09-935-727-5
13	579	98.6	455	9	US-09-898-234-2
14	579	98.6	455	9	US-09-898-234-17
15	579	98.6	455	9	US-09-756-854-5

16	579	98.6	455	9	US-09-899-429A-2	Sequence 2, Appli
17	579	98.6	455	9	US-09-899-429A-27	Sequence 27, Appl
18	579	98.6	455	9	US-09-792-356-2	Sequence 2, Appli
19	579	98.6	455	9	US-09-792-356-17	Sequence 17, Appl
20	579	98.6	455	10	US-09-314-889-5	Sequence 5, Appli
21	579	98.6	455	10	US-09-945-505-3	Sequence 3, Appli
22	579	98.6	455	12	US-10-099-007A-13	Sequence 13, Appl
23	579	98.6	455	13	US-10-005-842-3	Sequence 3, Appli
24	579	98.6	455	13	US-10-120-397-2	Sequence 2, Appli
25	579	98.6	455	13	US-10-041-574-5	Sequence 5, Appli
26	579	98.6	455	14	US-10-252-408-4	Sequence 4, Appli
27	579	98.6	455	14	US-10-038-557A-16	Sequence 16, Appl
28	579	98.6	455	14	US-10-175-902-4	Sequence 4, Appli
29	579	98.6	455	14	US-10-186-643-3	Sequence 3, Appli
30	579	98.6	455	14	US-10-189-189-5	Sequence 5, Appli
31	579	98.6	455	15	US-10-375-680-3	Sequence 3, Appli
32	579	98.6	455	15	US-10-418-242-5	Sequence 5, Appli
33	579	98.6	455	15	US-10-440-464-59	Sequence 59, Appl
34	579	98.6	909	14	US-10-226-296-4	Sequence 4, Appli
35	579	98.6	909	14	US-10-226-318-4	Sequence 4, Appli
36	421	71.7	471	9	US-09-970-532-2	Sequence 2, Appli
37	404	68.8	78	9	US-09-887-879-16	Sequence 16, Appl
38	404	68.8	78	9	US-09-992-964-16	Sequence 16, Appl
39	404	68.8	78	12	US-10-207-295-10	Sequence 10, Appl
40	404	68.8	78	13	US-10-112-793-23	Sequence 23, Appl
41	404	68.8	78	14	US-10-242-383-16	Sequence 16, Appl
42	384	65.4	461	9	US-09-899-422-15	Sequence 15, Appl
43	384	65.4	461	9	US-09-898-234-15	Sequence 15, Appl
44	384	65.4	461	9	US-09-899-429A-25	Sequence 25, Appl
45	384	65.4	461	9	US-09-792-356-15	Sequence 15, Appl

ALIGNMENTS

RESULT 1  
US-10-043-487-301  
; Sequence 301, Application US/10043487  
; Publication No. US20030055220A1  
; GENERAL INFORMATION:  
; APPLICANT: HYBRIGENICS  
; APPLICANT: Pierre, LEGRAIN  
; TITLE OF INVENTION: Protein-protein interactions between Shigella Flexneri polypeptic  
; TITLE OF INVENTION: mammalian polypeptides  
; FILE REFERENCE: B4778A  
; CURRENT APPLICATION NUMBER: US/10/043,487  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/261,130  
; PRIOR FILING DATE: 2001-01-12  
; NUMBER OF SEQ ID NOS: 561  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 301  
; LENGTH: 158  
; TYPE: PRT  
; ORGANISM: Shigella Flexneri  
US-10-043-487-301

Query Match	98.6%	Score 579;	DB 14;	Length 158;
Best Local Similarity	99.1%	Pred. No. 3.6e-58;		
Matches 110;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	2	AHKPQSLDTPATLYAVVENVPLRWKEFVKRLGLSDHEIDRLQLNGRCLREAYQYSML	61	
Db	48	AHKPQSLDTPATLYAVVENVPLRWKEFVKRLGLSDHEIDRLQLNGRCLREAYQYSML	107	
Qy	62	ATWRRTPRREATLELGRVLRDMDLLGCLDIEEALCGPAALPPAPSLR	112	
Db	108	ATWRRTPRREATLELGRVLRDMDLLGCLDIEEALCGPAALPPAPSLR	158	

RESULT 2  
US-10-349-977-37  
; Sequence 37, Application US/10349977











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; Sequence 17, Application US/09899422
; Patent No. US20020090676A1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
; APPLICANT: Himmler, Adolph
; APPLICANT: Maurer-Fogy, Ingrid
; APPLICANT: Stratowa, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
; TITLE OF INVENTION: Them
; FILE REFERENCE: 98,385-H
; CURRENT APPLICATION NUMBER: US/09/899,422
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 09/525,998
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 08/383,676
; PRIOR FILING DATE: 1995-02-01
; PRIOR APPLICATION NUMBER: 08/153,287
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: 07/821,750
; PRIOR FILING DATE: 1992-01-02
; PRIOR APPLICATION NUMBER: 07/511,430
; PRIOR FILING DATE: 1990-04-20
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: human TNF-R in
; OTHER INFORMATION: lTNF-R2
US-09-899-422-17

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Best Local Similarity 99.1%; Pred. No. 1.3e-57;
Matches 110; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db      345 AHKPSLDTDDPATLYAVVENVPLRWKEFVKRLGLSDHEIDRLQLNGRCLREAQYSML 404

QY      62 ATWRRTPRREATLELLGRVLRMDLLGCLDIEEALCGPAALPPAPSLLR 112
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RESULT 12
US-09-935-727-5
; Sequence 5, Application US/09935727
; Patent No. US20020150583A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta
; FILE REFERENCE: PF454P2
; CURRENT APPLICATION NUMBER: US/09/935,727
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/303,224
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: 60/252,131
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: 60/227,598
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: 09/518,931
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/168,235
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 60/146,371
; PRIOR FILING DATE: 1999-08-02
; PRIOR APPLICATION NUMBER: 60/131,964
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: 60/131,270
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/124,092
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; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/121,774
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: 09/006,352
; PRIOR FILING DATE: 1998-01-13
; PRIOR APPLICATION NUMBER: 60/035,496
; PRIOR FILING DATE: 1997-01-14
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-727-5

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QY      62 ATWRRTPRREATLELLGRVLRMDLLGCLDIEEALCGPAALPPAPSLLR 112
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RESULT 13
US-09-898-234-2
; Sequence 2, Application US/09898234
; Patent No. US20020155112A1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
; APPLICANT: Himmler, Adolph
; APPLICANT: Maurer-Fogy, Ingrid
; APPLICANT: Stratowa, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
; TITLE OF INVENTION: Them
; FILE REFERENCE: 98,385-I
; CURRENT APPLICATION NUMBER: US/09/898,234
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 09/525,998
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 08/383,676
; PRIOR FILING DATE: 1995-02-01
; PRIOR APPLICATION NUMBER: 08/153,287
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: 07/821,750
; PRIOR FILING DATE: 1992-01-02
; PRIOR APPLICATION NUMBER: 07/511,430
; PRIOR FILING DATE: 1990-04-20
; NUMBER OF SEQ ID NOS: 87
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; SEQ ID NO 2
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-898-234-2

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Best Local Similarity 99.1%; Pred. No. 1.3e-57;
Matches 110; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY      62 ATWRRTPRREATLELLGRVLRMDLLGCLDIEEALCGPAALPPAPSLLR 112
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Db      405 ATWRRTPRREATLELLGRVLRMDLLGCLDIEEALCGPAALPPAPSLLR 455
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GenCore version 5.1.6  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	579	98.6	455	1	GQHUT1	tumor necrosis fac
2	459.5	78.3	461	2	JC4302	tumor necrosis fac
3	384	65.4	461	1	GQRTT1	tumor necrosis fac
4	347.5	59.2	454	1	GQMST1	tumor necrosis fac
5	88.5	15.1	671	2	T09479	serine/threonine p
6	87	14.8	656	2	I49299	receptor interacti
7	83	14.1	1848	2	S37771	ankyrin, erythrocy
8	83	14.1	1862	2	I49502	ankyrin - mouse
9	82	14.0	163	2	B72550	probable methylmal
10	77.5	13.2	591	2	T41531	activator of Hsp70
11	77.5	13.2	591	2	T51996	hypothetical prote
12	77.5	13.2	1765	2	T42714	ankyrin 3, splice
13	77.5	13.2	1940	2	T42715	ankyrin 3, splice
14	77.5	13.2	1943	2	T42713	ankyrin 3, splice
15	77.5	13.2	1961	2	T42716	ankyrin 3, splice
16	77.5	13.2	4377	2	A55575	ankyrin 3, long sp
17	77	13.1	316	2	D83192	acetyl-coenzyme A
18	77	13.1	1856	2	B35049	ankyrin 1, erythro
19	77	13.1	1880	2	A35049	ankyrin 1, erythro
20	77	13.1	1881	1	SJHUK	ankyrin 1, erythro
21	76.5	13.0	388	2	E95177	aminotransferase,
22	76	12.9	536	2	D83419	probable ATP-bindi
23	73.5	12.5	580	2	G82693	glutaminyl-tRNA sy
24	72.5	12.4	138	2	S37773	ankyrin, erythrocy
25	72.5	12.4	295	2	A86745	conserved hypothet
26	72.5	12.4	388	2	G98043	aminotransferase (
27	72	12.3	1882	1	GNVUTR	genome polyprotein
28	71.5	12.2	156	2	D39109	genome polyprotein
29	71.5	12.2	208	2	A56912	FADD protein - hum

30	71.5	12.2	426	2	I48379	gene hb protein -
31	71.5	12.2	902	2	A55543	cmaA protein - Pse
32	71.5	12.2	3924	2	S37431	ankyrin 2, neurona
33	71	12.1	812	2	A83379	glycogen phosphory
34	70.5	12.0	402	2	E71279	hypothetical prote
35	70.5	12.0	412	2	E88736	protein F33D4.6a l
36	70.5	12.0	529	2	F84106	hypothetical prote
37	70.5	12.0	672	2	T32557	hypothetical prote
38	70.5	12.0	1083	2	S54293	regulator protein
39	70.5	12.0	1805	2	A34736	nestin - rat
40	70	11.9	533	2	G75348	conserved hypothet
41	70	11.9	643	2	E83142	probable transcrip
42	69.5	11.8	323	2	AD2753	lipoic Acid Synthet
43	69.5	11.8	323	2	E97534	lipoic acid synthet
44	69.5	11.8	395	2	F90012	hypothetical prote
45	69.5	11.8	446	2	AD3460	UDP-N-acetylglucos

ALIGNMENTS

RESULT 1

GQHUT1

tumor necrosis factor receptor 1 precursor [validated] - human  
N;Alternate names: P55 tumor necrosis factor receptor; TNF receptor type 1  
N;Contains: tumor necrosis factor alpha inhibitor; tumor necrosis factor binding protein  
C;Species: Homo sapiens (man)  
C;Date: 30-Jun-1992 #sequence revision 30-Jun-1992 #text change 08-Dec-2000  
C;Accession: A38208; A34899; A34900; A36555; C36555; A38281; S12057; JT0758; A60231; A38  
R;Fuchs, P.; Strehl, S.; Dworzak, M.; Himmler, A.; Ambros, P.F.  
Genomics 13, 219-224, 1992

A;Title: Structure of the human TNF receptor 1 (p60) gene (TNRF1) and localization to ch  
A;Reference number: A38208; MUID:92250049; PMID:1315717  
A;Accession: A38208

A;Molecule type: DNA

A;Residues: 1-455 <FUC>

A;Cross-references: GB:M75864; GB:M75865; GB:M75866; NID:g339748; PIDN:AAA61201.1; PID:g  
R;Loetscher, H.; Pan, Y.C.E.; Laht, H.W.; Gentz, R.; Brockhaus, M.; Tabuchi, H.; Lessl  
Cell 61, 351-359, 1990

A;Title: Molecular cloning and expression of the human 55 kd tumor necrosis factor recef  
A;Reference number: A34899; MUID:90235284; PMID:2158862

A;Accession: A34899

A;Molecule type: mRNA

A;Residues: 1-455 <LOE>

A;Cross-references: GB:M58286; GB:M33480; NID:g339753; PIDN:AAA36753.1; PID:g339754

A;Experimental source: placenta

A;Note: part of this sequence, including the amino end of the mature protein, confirmed  
R;Schall, T.J.; Lewis, M.; Koller, K.J.; Lee, A.; Rice, G.C.; Wong, G.H.W.; Gatanaga, T.  
Cell 61, 361-370, 1990

A;Title: Molecular cloning and expression of a receptor for human tumor necrosis factor.

A;Reference number: A34900; MUID:90235285; PMID:2158863

A;Accession: A34900

A;Molecule type: mRNA

A;Residues: 1-455 <SCH>

A;Cross-references: GB:M33294; NID:g339744; PIDN:AAA03210.1; PID:g339745

R;Himmler, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.; Pfizenmaier, K.; Lantz, M.;  
DNA Cell Biol. 9, 705-715, 1990

A;Title: Molecular cloning and expression of human and rat tumor necrosis factor recepto  
A;Reference number: A36555; MUID:91090841; PMID:1702293

A;Accession: A36555

A;Molecule type: mRNA

A;Residues: 1-455 <HIM>

A;Cross-references: GB:M63121; NID:g339755; PIDN:AAA36754.1; PID:g339756

A;Accession: C36555

A;Molecule type: protein

A;Residues: 30-38;41-53,'X',55-79,'XX',82-94,'NK','XX',100-104;107-128;162-167,'X',169-2  
A;Note: the purified protein, called tumor necrosis factor binding protein, is a soluble  
R;Gray, P.W.; Barrett, K.; Chantr, D.; Turner, M.; Feldmann, M.  
Proc. Natl. Acad. Sci. U.S.A. 87, 7380-7384, 1990

A;Title: Cloning of human tumor necrosis factor (TNF) receptor cDNA and expression of re  
A;Reference number: A38281; MUID:91017509; PMID:2170974

A;Accession: A38281

A;Molecule type: mRNA

A;Residues: 1-455 <GRA>  
A;Cross-references: GB:M37764  
A;Note: the authors translated the codon TGG for residue 371 as Thr, AAG for residue 372  
R;Nophar, Y.; Kemper, O.; Brakebusch, C.; Engelmann, H.; Zwang, R.; Aderka, D.; Holtmann  
EMBO J. 9, 3269-3278, 1990  
A;Title: Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA for the type  
I form of the receptor.  
A;Reference number: S12057; MUID:91006021; PMID:1698610  
A;Accession: S12057  
A;Molecule type: mRNA  
A;Residues: 1-455 <NOP>  
A;Cross-references: EMBL:X55313; NID:G37223; PIDN:CAA39021.1; PID:G37224  
A;Note: parts of soluble TNF binding protein 1, including its amino and carboxyl ends, w  
R;Kemper, O.; Wallach, D.  
Gene 134, 209-216, 1993  
A;Title: Cloning and partial characterization of the promoter for the human p55 tumor ne  
A;Reference number: JT0758; MUID:94085779; PMID:8262379  
A;Accession: JT0758  
A;Molecule type: DNA  
A;Residues: 1-13 <KEM>  
R;Seckinger, P.; Vey, E.; Turcatti, G.; Wingfield, P.; Dayer, J.M.  
Eur. J. Immunol. 20, 1167-1174, 1990  
A;Title: Tumor necrosis factor inhibitor: purification, NH-2-terminal amino acid sequenc  
A;Reference number: A60231; MUID:90292116; PMID:2113477  
A;Accession: A60231  
A;Molecule type: protein  
A;Residues: 41-43, 'X', 45-53, 'X', 55-57 <SEC>  
R;Gatanaga, T.; Hwang, C.; Kohr, W.; Cappuccini, F.; Lucci III, J.A.; Jeffes, E.W.B.; Le  
Proc. Natl. Acad. Sci. U.S.A. 87, 8781-8784, 1990  
A;Title: Purification and characterization of an inhibitor (soluble tumor necrosis facto  
tients.  
A;Reference number: A38258; MUID:91062364; PMID:2174164  
A;Accession: A38258  
A;Molecule type: protein  
A;Residues: 41-60 <GAT>  
A;Experimental source: cancer patient serum  
R;Olsson, I.; Lantz, M.; Nilsson, E.; Peetre, C.; Thysell, H.; Grubb, A.; Adolf, G.  
Eur. J. Haematol. 42, 270-275, 1989  
A;Title: Isolation and characterization of a tumor necrosis factor binding protein from  
A;Reference number: A60594; MUID:89171156; PMID:2924890  
A;Accession: A60594  
A;Molecule type: protein  
A;Residues: 41-43, 'X', 45-53, 'V', 55-57, 'XK', 60 <OLS>  
A;Experimental source: renal failure patient urine  
R;Engelmann, H.; Novick, D.; Wallach, D.  
J. Biol. Chem. 265, 1531-1536, 1990  
A;Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence  
A;Reference number: A35010; MUID:90110215; PMID:2153136  
A;Accession: A35010  
A;Molecule type: protein  
A;Residues: 41-45 <ENG>  
A;Experimental source: normal urine  
R;Kajihara, J.; Asada, A.; Kiriwara, S.; Kato, K.  
Biosci. Biotechnol. Biochem. 58, 2266-2268, 1994  
A;Title: Amino acid sequence of natural tumor necrosis factor alpha inhibitor purified f  
A;Reference number: JC2404; MUID:95128033; PMID:7765720  
A;Accession: JC2404  
A;Molecule type: protein  
A;Residues: 41-53, 'X', 55-144, 'X', 146-150, 'X', 152-186, 'X', 188-201 <KAJ>  
A;Experimental source: urine  
C;Comment: This protein is one of two known receptors for both TNF-alpha (cachectin) and  
C;Genetics:  
A;Gene: GDB:TNFR1  
A;Cross-references: GDB:125913; OMIM:191190  
A;Map position: 12p13.2-12p13.2  
A;Introns: 13/3; 65/1; 108/1; 158/1; 184/2; 209/1; 247/1; 256/3; 353/1  
C;Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology  
C;Keywords: duplication; glycoprotein; receptor; transmembrane protein  
F;1-21/Domain: signal sequence #status predicted <SIG>  
F;22-455/Product: tumor necrosis factor receptor 1 #status predicted <MAT>  
F;30-211/Domain: extracellular #status predicted <EXT>  
F;41-201/Product: TNF binding protein 1 (tumor necrosis factor alpha inhibitor) #status  
F;44-82/Domain: NGF receptor repeat homology <NGL>

F;84-126/Domain: NGF receptor repeat homology <NG2>  
F;127-167/Domain: NGF receptor repeat homology <NG3>  
F;168-196/Domain: NGF receptor repeat homology <NG4>  
F;212-234/Domain: transmembrane #status predicted <MEM>  
F;235-455/Domain: intracellular #status predicted <INT>  
F;54,145,151/Binding site: carboxylate (Asn) (covalent) #status predicted  
Query Match 98.6%; Score 579; DB 1; Length 455;  
Best Local Similarity 99.1%; Pred. No. 5.3e-52;  
Matches 110; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 2 AHKQSLDTDDPATLYAVVENVPPLRWKEFVKRLGLSDHEIDRLQLNGRCLREAQYSML 61  
Db |||||  
345 AHKQSLDTDDPATLYAVVENVPPLRWKEFVKRLGLSDHEIDRLQLNGRCLREAQYSML 404  
QY 62 ATWRRRTPRREATLELLGRVLRMDMLLGCLIEDIEEALCGPAALPPAPSLLR 112  
Db |||||  
405 ATWRRRTPRREATLELLGRVLRMDMLLGCLIEDIEEALCGPAALPPAPSLLR 455  
RESULT 2  
JC4302  
tumor necrosis factor receptor p55 precursor - pig  
C;Species: Sus scrofa domestica (domestic pig)  
C;Date: 29-Nov-1995 #sequence\_revision 08-Feb-1996 #text\_change 23-Jul-1999  
C;Accession: JC4302; PC4093  
R;Suter, B.; Pauli, U.  
Gene 163, 263-266, 1995  
A;Title: Cloning of the cDNA encoding the porcine p55 tumor necrosis factor receptor.  
A;Reference number: JC4302; MUID:96011645; PMID:7590278  
A;Accession: JC4302  
A;Molecule type: mRNA  
A;Residues: 1-461 <SUT>  
A;Cross-references: GB:U19994; NID:G1141752; PIDN:AAC48499.1; PID:G1141753  
A;Accession: PC4093  
A;Molecule type: protein  
A;Residues: 1-7 <SU2>  
A;Experimental source: kidney cell line 15  
C;Genetics:  
A;Gene: tnfr  
C;Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology  
C;Keywords: glycoprotein; kidney; receptor; transmembrane protein; tumor  
F;1-29/Domain: signal sequence #status predicted <SIG>  
F;30-461/Product: tumor necrosis factor receptor p55 #status predicted <MAT>  
F;44-194/Domain: extracellular cysteine rich #status predicted <EXT>  
F;44-82/Domain: NGF receptor repeat homology <NGL>  
F;84-126/Domain: NGF receptor repeat homology <NGF>  
F;211-231/Domain: transmembrane #status predicted <TMM>  
F;361-447/Domain: signal transduction #status predicted <SIT>  
F;54,145,151/Binding site: carboxylate (Asn) (covalent) #status predicted  
Query Match 78.3%; Score 459.5; DB 2; Length 461;  
Best Local Similarity 82.1%; Pred. No. 1.2e-39;  
Matches 92; Conservative 4; Mismatches 15; Indels 1; Gaps 1;  
QY 2 AHK-QS-LD-TD-DPAT-LY-AV-VEN-V-P-L-R-W-K-E-F-V-K-R-L-G-L-S-D-H-E-I-D-R-L-Q-L-N-G-R-C-L-R-E-A-Q-Y-S-M-L 60  
Db |||||  
350 AHSAPAQADADPATLYAVVDGVPTRWKEFVRRRLGLSEHEIERLELQNGRCLREAQYSM 409  
QY 61 LATWRRRTPRREATLELLGRVLRMDMLLGCLIEDIEEALCGPAALPPAPSLLR 112  
Db |||||  
410 LAEWRRTSRREATLELLGSVLRMDMLLGCLIEDIEEALRGPARLAPAPHLR 461  
RESULT 3  
GQRTT1  
tumor necrosis factor receptor 1 precursor - rat  
N;Contains: tumor necrosis factor binding protein 1 (TNF blocking factor)  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 30-Jun-1992 #sequence\_revision 07-Oct-1994 #text\_change 22-Jun-1999  
C;Accession: B36555  
R;Himmeler, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.; Pfizenmaier, K.; Lantz, M.;  
DNA Cell Biol. 9, 705-715, 1990



A;Title: Molecular cloning and expression of human and rat tumor necrosis factor receptor  
A;Reference number: A36555; MUID:91090841; PMID:1702293  
A;Accession: B36555  
A;Molecule type: mRNA  
A;Residues: 1-461 <HIM>  
A;Cross-references: GB:M631122; NID:g207361; PIDN:AAA42256.1; PID:g207362  
C;Comment: This protein is one of two known receptors for both TNF-alpha (cachectin) and C;Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology  
C;Keywords: duplication; glycoprotein; receptor; transmembrane protein  
F;1-29/Domain: signal sequence #status predicted <SIG>  
F;30-461/Product: tumor necrosis factor receptor type 1 #status predicted <MAT>  
F;30-211/Domain: extracellular #status factor predicted <EXT>  
F;30-201/Product: tumor necrosis factor binding protein #status predicted <TBP>  
F;44-82/Domain: NGF receptor repeat homology <NG1>  
F;84-126/Domain: NGF receptor repeat homology <NG2>  
F;127-167/Domain: NGF receptor repeat homology <NG3>  
F;168-204/Domain: NGF receptor repeat homology <NG4>  
F;212-234/Domain: transmembrane #status predicted <MEM>  
F;235-461/Domain: intracellular #status predicted <INT>  
F;54,151,201/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 65.4%; Score 384; DB 1; Length 461;  
Best Local Similarity 71.6%; Pred. No. 7.5e-32;  
Matches 73; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

QY 1 MAHKPQSLDTPATLYAVVENVPPLRWKEFVKRLGLSDHEIDRLQLNGRCLREAHYSM 60  
Db 351 VAAQPQRLDTADPAMLYAVVDGVPPTRWKEFMRLLGLSEHEIERLELQNGRCLREAHYSM 410

QY 61 LATWRRTPRREATLELLGRVLRDMDLLGCLEDIEEALCGPA 102  
Db 411 LEAWRRTPRHEATLDVVGRLVCLDMNLRGCLENIRETLESPA 452

RESULT 4

GOMST1  
tumor necrosis factor receptor 1 precursor - mouse  
N;Alternate names: tumor necrosis factor receptor, 55K  
C;Species: Mus musculus (house mouse)  
C;Date: 30-Jun-1992 #sequence revision 30-Jun-1992 #text\_change 01-Dec-2000  
C;Accession: A38634; B40254; S16677; S19021; I54532; I57826  
R;Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, E. Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991  
A;Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis factor  
A;Reference number: A38634; MUID:91187885; PMID:1849278  
A;Accession: A38634  
A;Molecule type: mRNA  
A;Residues: 1-454 <LEW>  
A;Cross-references: GB:M60468; NID:g199825; PIDN:AAA39751.1; PID:g199826  
R;Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; Jenk Mol. Cell. Biol. 11, 3020-3026, 1991  
A;Title: Molecular cloning and expression of the type 1 and type 2 murine receptors for A;Reference number: A40254; MUID:91246168; PMID:1645445  
A;Accession: B40254  
A;Molecule type: mRNA  
A;Residues: 1-454 <GO2>  
A;Cross-references: GB:M60468; NID:g199825; PIDN:AAA39751.1; PID:g199826  
R;Barrett, K.; Taylor-Fishwick, D.A.; Cope, A.P.; Kissnerghis, A.M.; Gray, P.W.; Feldma Eur. J. Immunol. 21, 1649-1656, 1991  
A;Title: Cloning, expression and cross-linking analysis of the murine p55 tumor necrosis A;Reference number: S16677; MUID:91285014; PMID:1647956  
A;Accession: S16677  
A;Molecule type: mRNA  
A;Residues: 1-454 <BAR>  
A;Cross-references: EMBL:X59238; NID:g53578; PIDN:CAA41922.1; PID:g53579  
R;Rothe, J.G.; Brockhaus, M.; Gentz, R.; Lesslauer, W. Immunogenetics 34, 338-340, 1991  
A;Title: Molecular cloning and expression of the mouse Tnf receptor type b. A;Reference number: S19021; MUID:92039815; PMID:1657766  
A;Accession: S19021  
A;Molecule type: mRNA  
A;Residues: 1-454 <ROT>  
A;Cross-references: EMBL:X57796; NID:g54848; PIDN:CAA40936.1; PID:g54849

R;Bebo, B.F. Immunogenetics 39, 450-451, 1994  
A;Title: Nucleotide sequence of the TNF type I receptor from a mouse endothelioma cell 1 A;Reference number: I54532; MUID:94245292; PMID:8188324  
A;Accession: I54532  
A;Status: translated from GB/EMBL/DDBJ  
A;Molecule type: mRNA  
A;Residues: 1-454 <RES>  
A;Cross-references: GB:L26349; NID:g430732; PIDN:AAA59361.1; PID:g430733  
R;Rothe, J.G.; Bluethmann, H.; Gentz, R.; Lesslauer, W.; Steinmetz, M. Mol. Immunol. 30, 165-176, 1993  
A;Title: Genomic organization and promoter function of the murine tumor necrosis factor A;Reference number: I57826; MUID:93156721; PMID:8381516  
A;Accession: I57826  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-393,'G',395-454 <RE2>  
A;Cross-references: GB:M76656; NID:g202100; PIDN:AAA40465.1; PID:g202102  
C;Comment: This protein is one of two distantly related receptors for both TNF-alpha (ca C;Genetics:  
A;Gene: TNFR-2  
A;Introns: 13/3; 65/1; 108/1; 158/1; 184/2; 210/1; 248/1; 257/3; 353/1  
C;Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology  
C;Keywords: cytokine receptor; duplication; glycoprotein; receptor; transmembrane protei F;1-29/Domain: signal sequence #status predicted <SIG>  
F;30-454/Product: tumor necrosis factor receptor type 1 #status predicted <MAT>  
F;30-212/Domain: extracellular #status predicted <EXT>  
F;44-82/Domain: NGF receptor repeat homology <NG1>  
F;84-126/Domain: NGF receptor repeat homology <NG2>  
F;127-167/Domain: NGF receptor repeat homology <NG3>  
F;168-204/Domain: NGF receptor repeat homology <NG4>  
F;213-235/Domain: transmembrane #status predicted <MEM>  
F;236-454/Domain: intracellular #status predicted <INT>  
F;54,151,202/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 59.2%; Score 347.5; DB 1; Length 454;  
Best Local Similarity 68.3%; Pred. No. 4.4e-28;  
Matches 69; Conservative 11; Mismatches 20; Indels 1; Gaps 1;

QY 2 AHKPQSLDTPATLYAVVENVPPLRWKEFVKRLGLSDHEIDRLQLNGRCLREAHYSML 61  
Db 346 AH-PQRPDNADLAILYAVVDGVPPTRWKEFMRMGLSEHEIERLEMQNGRCLREAHYSML 404

QY 62 ATWRRTPRREATLELLGRVLRDMDLLGCLEDIEEALCGPA 102  
Db 405 EAWRRTPRHEDTLEVVLVLSKMNLAGCLENILEALRNPA 445

RESULT 5

T09479  
serine/threonine protein kinase (EC 2.7.1.1-) RIP - human  
C;Species: Homo sapiens (man)  
C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 17-Nov-2000  
C;Accession: T09479; I38992  
R;Huang, J.; Hsu, H.; Baichwal, V.R.; Goeddel, D.V. submitted to the EMBL Data Library, August 1998  
A;Reference number: Z16685  
A;Accession: T09479  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: mRNA  
A;Residues: 1-671 <HUA>  
A;Cross-references: EMBL:U50062; NID:g3426026; PID:g3426027  
R;Stanger, B.Z.; Leder, P.; Lee, T.H.; Kim, E.; Seed, B. Cell 81, 513-523, 1995  
A;Title: RIP: a novel protein containing a death domain that interacts with Fas/APO-1 (C A;Reference number: A56913; MUID:95277838; PMID:7538908  
A;Accession: I38992  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 300-513,'S',515-671 <RES>  
A;Cross-references: EMBL:U25994; NID:g829616; PIDN:AAC50137.1; PID:g829617  
C;Genetics:  
A;Gene: RIP

C;Keywords: ATP binding; phosphotransferase

Query Match 15.1%; Score 88.5; DB 2; Length 671;  
Best Local Similarity 27.0%; Pred. No. 0.39;  
Matches 27; Conservative 18; Mismatches 36; Indels 19; Gaps 4;  
QY 11 DDPAATLYAVW-----ENVPPLR-----WKEFVKRLGLSDHEIDRLQLNGR-CLR 54  
Db 566 EEPAAKYQAIFDNTTSLTDKHLDPIRENLGKHKNCAKLGFTQSQIDEIDHYERDGLK 625  
QY 55 EAQYSMLATWRRRTPPREATLELLGRVLRD---MDLLGCL 91  
Db 626 EKVYQMLQKWMREGIKGATVGKLAQALHQCSTRIDLLSSL 665

RESULT 6  
I49299  
receptor interacting protein RIP - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 09-Mar-1996 #sequence\_revision 09-Mar-1996 #text\_change 05-Nov-1999  
C;Accession: I49299  
R;Stanger, B.Z.; Leder, P.; Lee, T.H.; Kim, E.; Seed, B.  
Cell 81, 513-523, 1995  
A;Title: RIP: a novel protein containing a death domain that interacts with Fas/APO-1 (CD95)  
A;Reference number: A56913; MUID:95277838; PMID:7538908  
A;Accession: I49299  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-656 <RES>  
A;Cross-references: EMBL:U25995; NID:g829618; PIDN:AAB60487.1; PID:g829619  
C;Genetics:  
A;Gene: RIP  
C;Superfamily: protein kinase homology  
F;15-293/Domain: protein kinase homology <KIN>

Query Match 14.8%; Score 87; DB 2; Length 656;  
Best Local Similarity 30.9%; Pred. No. 0.54;  
Matches 25; Conservative 15; Mismatches 31; Indels 10; Gaps 3;  
QY 21 ENVPPLR-----WKEFVKRLGLSDHEIDRLQLNGR-CLREAQYSMLATWRRRTPPREA 73  
Db 570 EHLNPIRENLRQWNCARKLGFTESQIDEIDHYERDGLKEKVKYQMLQKWMREGTKGA 629  
QY 74 TLELLGRVLRD---MDLLGCL 91  
Db 630 TVGKLAQALHQCSTRIDLLNHL 650

RESULT 7  
S37771  
ankyrin, erythrocyte - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 27-May-1994 #sequence\_revision 03-Aug-1995 #text\_change 13-Aug-1999  
C;Accession: S37771  
R;Birkenmeier, C.S.; White, R.A.; Peters, L.L.; Hall, E.J.; Lux, S.E.; Barker, J.E.  
J. Biol. Chem. 268, 9533-9540, 1993  
A;Title: Complex patterns of sequence variation and multiple 5' and 3' ends are found among the 5' ends of ankyrin repeat homology regions of the regulatory do  
A;Reference number: S37771; MUID:93252825; PMID:8486643  
A;Accession: S37771  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-1848 <BIR>  
A;Cross-references: EMBL:X69063; NID:g311816; PIDN:CAA48801.1; PID:g311817  
C;Superfamily: ankyrin; ankyrin repeat homology  
C;Keywords: alternative splicing  
F;48-80/Domain: ankyrin repeat homology <AN01>  
F;81-113/Domain: ankyrin repeat homology <AN02>  
F;114-146/Domain: ankyrin repeat homology <AN03>  
F;147-175/Domain: ankyrin repeat homology <AN04>  
F;176-208/Domain: ankyrin repeat homology <AN05>  
F;209-241/Domain: ankyrin repeat homology <AN06>  
F;242-274/Domain: ankyrin repeat homology <AN07>  
F;275-307/Domain: ankyrin repeat homology <AN08>

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F;341-373/Domain: ankyrin repeat homology <AN10>  
F;374-406/Domain: ankyrin repeat homology <AN11>  
F;407-439/Domain: ankyrin repeat homology <AN12>  
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F;473-505/Domain: ankyrin repeat homology <AN14>  
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F;539-571/Domain: ankyrin repeat homology <AN16>  
F;572-604/Domain: ankyrin repeat homology <AN17>  
F;605-637/Domain: ankyrin repeat homology <AN18>  
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F;671-703/Domain: ankyrin repeat homology <AN20>  
F;704-736/Domain: ankyrin repeat homology <AN21>  
F;737-769/Domain: ankyrin repeat homology <AN22>  
F;770-802/Domain: ankyrin repeat homology <AN23>  
Query Match 14.1%; Score 83; DB 2; Length 1848;  
Best Local Similarity 22.6%; Pred. No. 4.6;  
Matches 31; Conservative 20; Mismatches 48; Indels 38; Gaps 4;  
QY 9 DTDDPATLYAVVENVPPLRWKEFVKRLGLSDHEIDRLQLNGRCLREAQYSMLATWRRRT 68  
Db 1411 DTDREVEMRAVIREHGLSLWAELARELQFVEDINRIVENPNSLDQSTALLTLWVDR- 1469  
QY 69 PRREATLELLGRVLRDMD---LLGCL 94  
Db 1470 EGENAKMENLYTALRNIDRSEIVNMLEVSGRQSRNLKPERRHGDREYSLSPSQVNGYSSL 1529  
QY 95 EEALCGPAALP---PAP 108  
Db 1530 QDELLSPASLQYALPSP 1546  
RESULT 8  
I49502  
ankyrin - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 13-Aug-1999  
C;Accession: I49502  
R;White, R.A.; Birkenmeier, C.S.; Peters, L.L.; Barker, J.E.; Lux, S.E.  
Mamm. Genome 3, 281-285, 1992  
A;Title: Murine erythrocyte ankyrin cDNA: Highly conserved regions of the regulatory do  
A;Reference number: I49502; MUID:92345717; PMID:1386265  
A;Accession: I49502  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: mRNA  
A;Residues: 1-1862 <RES>  
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C;Genetics:  
A;Gene: Ank-1  
C;Superfamily: ankyrin; ankyrin repeat homology  
C;Keywords: alternative splicing  
F;40-72/Domain: ankyrin repeat homology <AN01>  
F;73-105/Domain: ankyrin repeat homology <AN02>  
F;106-138/Domain: ankyrin repeat homology <AN03>  
F;139-167/Domain: ankyrin repeat homology <AN04>  
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F;201-233/Domain: ankyrin repeat homology <AN06>  
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F;267-299/Domain: ankyrin repeat homology <AN08>  
F;300-332/Domain: ankyrin repeat homology <AN09>  
F;333-365/Domain: ankyrin repeat homology <AN10>  
F;366-398/Domain: ankyrin repeat homology <AN11>  
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F;498-530/Domain: ankyrin repeat homology <AN15>  
F;531-563/Domain: ankyrin repeat homology <AN16>  
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F;597-629/Domain: ankyrin repeat homology <AN18>  
F;630-662/Domain: ankyrin repeat homology <AN19>  
F;663-695/Domain: ankyrin repeat homology <AN20>  
F;696-728/Domain: ankyrin repeat homology <AN21>







GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 1, 2004, 14:33:56 ; Search time 8.0479 Seconds  
(without alignments)  
724.643 Million cell updates/sec

Title: US-09-854-906-1  
Perfect score: 587  
Sequence: 1 MAHKPQSLDTDDPATLYAVV.....DIEEALCGPAALPPAPSLLR 112

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	579	98.6	455	1	TR1A_HUMAN
2	459.5	78.3	461	1	TR1A_PIG
3	421	71.7	471	1	TR1A_BOVIN
4	384	65.4	461	1	TR1A_RAT
5	347.5	59.2	454	1	TR1A_MOUSE
6	164.5	28.0	417	1	TR25_HUMAN
7	97	16.5	381	1	T10B_MOUSE
8	88.5	15.1	671	1	RIK1_HUMAN
9	87	14.8	656	1	RIK1_MOUSE
10	83	14.1	1862	1	ANK1_MOUSE
11	77.5	13.2	591	1	ST11_SCHPO
12	77.5	13.2	4377	1	ANK3_HUMAN
13	77	13.1	1880	1	ANK1_HUMAN
14	73.5	12.5	440	1	T10B_HUMAN
15	73.5	12.5	580	1	SYQ_XYLFA
16	73	12.4	1199	1	Y173_HUMAN
17	72.5	12.4	295	1	YJIE_LACLA
18	72	12.3	1882	1	POL2_TRSVR
19	71.5	12.2	208	1	FADD_HUMAN
20	71.5	12.2	580	1	SYQ_XYLFT
21	71.5	12.2	1092	1	RHG7_MOUSE
22	71.5	12.2	3924	1	ANK2_HUMAN
23	70.5	12.0	1091	1	RHG7_RAT
24	70.5	12.0	1805	1	NEST_RAT
25	69.5	11.8	323	1	LIPA_AGR75
26	69.5	11.8	354	1	HOM1_HUMAN
27	69.5	11.8	429	1	MURA_BRUME
28	69.5	11.8	1091	1	RHG7_HUMAN
29	69	11.8	481	1	TPH_XENLA
30	69	11.8	887	1	PMC2_MOUSE
31	68.5	11.7	2390	1	SPCP_HUMAN
32	68	11.6	445	1	TPH1_CHICK
33	68	11.6	521	1	ICEA_HUMAN

34	67.5	11.5	384	1	BRH2_RAT	O88181	rattus norv
35	67	11.4	885	1	PMC2_HUMAN	Q01780	homo sapien
36	66.5	11.3	189	1	YI35_PASMU	Q9ck03	pasteurella
37	66.5	11.3	366	1	HOM1_MOUSE	Q9z2y3	mus musculus
38	66.5	11.3	456	1	PYRC_MEITMA	Q8pvf4	methanosarc
39	66.5	11.3	467	1	YG3H_YEAST	P53285	saccharomyc
40	66.5	11.3	781	1	NANH_VIBCH	P37060	vibrio chol
41	66	11.2	1618	1	NEST_HUMAN	P48681	homo sapien
42	65.5	11.2	205	1	FADD_MOUSE	Q61160	mus musculus
43	65.5	11.2	322	1	LIPA_RHIME	Q92q94	rhizobium m
44	65	11.1	150	1	YAO2_SCHPO	Q10081	schizosacch
45	65	11.1	554	1	PYRG_CORGL	Q8ngl7	corynebacte

ALIGNMENTS

RESULT 1		TR1A_HUMAN		STANDARD;		PRT;		455 AA.	
ID	TR1A_HUMAN								
AC	P19438;								
DT	01-FEB-1991 (Rel. 17, Created)								
DT	01-FEB-1991 (Rel. 17, Last sequence update)								
DT	15-MAR-2004 (Rel. 43, Last annotation update)								
DE	Tumor necrosis factor receptor superfamily member 1A precursor (p60)								
DE	(TNF-R1) (TNF-RI) (p55) (CD120a) [Contains: Tumor necrosis factor								
DE	binding protein 1 (TBPI)]								
GN	TNFRSF1A OR TNFR1 OR TNFAR.								
OS	Homo sapiens (Human).								
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.								
OX	NCBI_TaxID=9606;								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RC	TISSUE=Placenta;								
RX	MEDLINE=90235285; PubMed=2158863;								
RA	Schall T.J., Lewis M., Koller K.J., Lee A., Rice G.C., Wong G.H.W.,								
RA	Getanaga T., Granger G.A., Lentz R., Raab H., Kohr W.J., Goeddel D.V.;								
RT	"Molecular cloning and expression of a receptor for human tumor								
RT	necrosis factor.";								
RL	Cell 61:361-370(1990).								
RN	[2]								
RP	SEQUENCE FROM N.A.								
RX	MEDLINE=90235284; PubMed=2158862;								
RA	Loetscher H., Pan Y.-C.E., Lahm H.-W., Gentz R., Brockhaus M.,								
RA	Tabuchi H., Lesslauer W.;								
RT	"Molecular cloning and expression of the human 55 kd tumor necrosis								
RT	factor receptor.";								
RL	Cell 61:351-359(1990).								
RN	[3]								
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 41-53; 110-124 AND 199-201.								
RX	MEDLINE=91006021; PubMed=1698610;								
RA	Nophar Y., Kemper O., Brakebusch C., Engelmann H., Zwang R.,								
RA	Aderka D., Holtmann H., Wallach D.;								
RT	"Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA								
RT	for the type I TNF-R, cloned using amino acid sequence data of its								
RT	soluble form, encodes both the cell surface and a soluble form of the								
RT	receptor.";								
RL	EMBO J. 9:3269-3278(1990).								
RN	[4]								
RP	SEQUENCE FROM N.A.								
RX	MEDLINE=91090841; PubMed=1702293;								
RA	Himmeler A., Maurer-Fogy I., Kroenke M., Scheurich P., Pfizenmaier K.,								
RA	Lantz M., Olsson I., Hauptmann R., Stratowa C., Adolf G.R.;								
RT	"Molecular cloning and expression of human and rat tumor necrosis								
RT	factor receptor chain (p60) and its soluble derivative, tumor								
RT	necrosis factor-binding protein.";								
RL	DNA Cell Biol. 9:705-715(1990).								
RN	[5]								
RP	SEQUENCE FROM N.A.								
RC	TISSUE=Placenta;								
RX	MEDLINE=91017509; PubMed=2170974;								
RA	Gray P.W., Barrett K., Chantry D., Turner M., Feldman M.;								

RT "Cloning of human tumor necrosis factor (TNF) receptor cDNA and  
RT expression of recombinant soluble TNF-binding protein.";  
RL Proc. Natl. Acad. Sci. U.S.A. 87:7380-7384(1990).  
RN [6]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92250049; PubMed=1315717;  
RA Fuchs P., Strehl S., Dworzak M., Himmler A., Ambros P.F.;  
RA "Structure of the human TNF receptor 1 (p60) gene (TNFR1) and  
RT localization to chromosome 12p13.";  
RL Genomics 13:219-224(1992).  
RN [7]  
RP SEQUENCE FROM N.A.  
RA Rieder M.J., Armel T.Z., Carrington D.P., Ozuna M., Kuldane S.A.,  
RA Rajkumar N.R., Toth E.J., Yi Q., Nickerson D.A.;  
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
RN [8]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Muscle;  
RX MEDLINE=2238257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length  
RT human and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [9]  
RP SEQUENCE OF 41-45.  
RX MEDLINE=90110215; PubMed=2153136;  
RA Engelmann H., Novick D., Wallach D.;  
RA "Two tumor necrosis factor-binding proteins purified from human  
RT urine. Evidence for immunological cross-reactivity with cell surface  
RT tumor necrosis factor receptors.";  
RL J. Biol. Chem. 265:1531-1536(1990).  
RN [10]  
RP INTERACTION WITH BAG4.  
RX MEDLINE=99115917; PubMed=9915703;  
RA Jiang Y., Woronicz J.D., Liu W., Goeddel D.V.;  
RA "Prevention of constitutive TNF receptor 1 signaling by silencer of  
RT death domains.";  
RL Science 283:543-546(1999).  
RN [11]  
RP X-RAY CRYSTALLOGRAPHY (2.85 ANGSTROMS) OF 30-211 IN COMPLEX WITH TNFB.  
RX MEDLINE=93258809; PubMed=8387891;  
RA Banner D.W., D'Arcy A., Janes W., Gentz R., Schoenfeld H.-J.,  
RA Broger C., Loetscher H., Lesslauer W.;  
RT "Crystal structure of the soluble human 55 kd TNF receptor-human TNF  
RT beta complex: implications for TNF receptor activation.";  
RL Cell 73:431-445(1993).  
RN [12]  
RP X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS) OF 41-202.  
RX MEDLINE=97094982; PubMed=8939750;  
RA Naismith J.H., Devine T.Q., Khono H., Sprang S.R.;  
RT "Structures of the extracellular domain of the type I tumor necrosis  
RT factor receptor.";  
RL Structure 4:1251-1262(1996).  
RN [13]  
RP VARIANTS FHF ARG-59; TYR-62; MET-79; PHE-81; ARG-117 AND TYR-117.  
RX MEDLINE=99213501; PubMed=10199409;  
RA McDermott M.F., Aksentijevich I., Galon J., McDermott E.M.,

RA Ogunkolade B.W., Centola M., Mansfield E., Gadina M., Karenko I.,  
RA Pettersson T., McCarthy J., Frucht D.M., Aringer M., Torosyan Y.,  
RA Teppo A.-M., Wilson M., Karaarslan H.M., Wan Y., Todd I., Wood G.,  
RA Schlingens R., Kumarajeewa T.R., Cooper S.M., Vella J.P., Amos C.I.,  
RA Mulley J., Quane K.A., Molloy M.G., Rnaki A., Powell R.J.,  
RA Hitman G.A., O'Shea J., Kastner D.L.;  
RT "Germline mutations in the extracellular domains of the 55 kDa TNF  
RT receptor, TNFR1, define a family of dominantly inherited  
RL autoinflammatory syndromes.";  
RL Cell 97:133-144(1999).  
CC -!- FUNCTION: Receptor for TNFSF2/TNF-alpha and homotrimeric  
CC TNFSF1/lymphotoxin-alpha. The adaptor molecule FADD recruits  
CC caspase-8 to the activated receptor. The resulting death-inducing  
CC signaling complex (DISC) performs caspase-8 proteolytic activation  
CC which initiates the subsequent cascade of caspases (aspartate-  
CC specific cysteine proteases) mediating apoptosis. Contributes to  
CC the induction of noncytotoxic TNF effects including anti-viral  
CC state and activation of the acid sphingomyelinase.  
CC -!- SUBUNIT: Binding of TNF to the extracellular domain leads to  
CC homotrimerization. The aggregated death domains provide a novel  
CC molecular interface that interacts specifically with the death  
CC domain of TRADD. Various TRADD-interacting proteins such as TRAFs,  
CC RIP and possibly FADD, are recruited to the complex by their  
CC association with TRADD. This complex activates at least two  
CC distinct signaling cascades, apoptosis and NF-kappa-B signaling.  
CC Binds BAG4.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein and secreted.  
CC -!- DOMAIN: The domain that induces A-SMASE is probably identical to  
CC the death domain. The N-SMASE activation domain (NSD) is both  
CC necessary and sufficient for activation of N-SMASE.  
CC -!- PTM: The soluble form is produced from the membrane form by  
CC proteolytic processing.  
CC -!- DISEASE: Defects in TNFRSF1A are a cause of autosomal dominant  
CC familial hibernian fever (FHF) [MIM:142680]. FHF is a disease  
CC characterized by recurrent fever, abdominal pain, localized tender  
CC skin lesions and myalgia.  
CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.  
CC -!- SIMILARITY: Contains 1 death domain.  
CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD120a entry;  
CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd120a.htm".  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; X55313; CAA39021.1; -.  
DR EMBL; M33294; AAA03210.1; -.  
DR EMBL; M58286; AAA36753.1; -.  
DR EMBL; M63121; AAA36754.1; -.  
DR EMBL; M75866; AAA61201.1; -.  
DR EMBL; M75864; AAA61201.1; JOINED.  
DR EMBL; M60275; AAA36756.1; -.  
DR EMBL; A21522; CAA01558.1; -.  
DR EMBL; AY131997; AAM77802.1; -.  
DR EMBL; BC010140; AAH10140.1; -.  
DR PIR; A38208; GQHUT1.  
DR PDB; 1TNR; 31-JUL-94.  
DR PDB; 1NCF; 07-DEC-95.  
DR PDB; 1EXT; 11-JAN-97.  
DR PDB; 1FT4; 12-OCT-01.  
DR PDB; 1ICH; 01-APR-02.  
DR Genew; HGNC:11916; TNFRSF1A.  
DR MIM; 191190; -.  
DR MIM; 142680; -.  
DR GO; GO:0005576; C:extracellular; TAS.  
DR GO; GO:0005887; C:integral to plasma membrane; TAS.  
DR GO; GO:0005032; F:tumor necrosis factor receptor cell differe. . ; TAS.  
DR GO; GO:0007165; P:signal transduction; TAS.







specific cysteine proteases) mediating apoptosis (By similarity).  
-!- SUBUNIT: Binding of TNF to the extracellular domain leads to homotrimerization. The aggregated death domains provide a novel molecular interface that interacts specifically with the death domain of TRADD. Various TRADD-interacting proteins such as TRAFs, RIP and possibly FADD, are recruited to the complex by their association with TRADD. This complex activates at least two distinct signaling cascades, apoptosis and NF-kappa-B signaling. Binds BAG4 (By similarity).  
-!- SUBCELLULAR LOCATION: Type I membrane protein.  
-!- SIMILARITY: Contains 4 TNFR-Cys repeats.  
-!- SIMILARITY: Contains 1 death domain.  
-----  
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EMBL; U90937; AAB65143.1; -.  
HSSP; P19438; 1TNR.  
InterPro; IPR000488; Death.  
InterPro; IPR001368; TNFR\_c6.  
Pfam; PF00531; death; 1.  
SMART; SM00005; DEATH; 1.  
SMART; SM00208; TNFR; 3.  
PROSITE; PS00652; TNFR\_NGFR\_1; 3.  
PROSITE; PS50050; TNFR\_NGFR\_2; 3.  
PROSITE; PS50017; DEATH\_DOMAIN; 1.  
Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.  
FT SIGNAL 1 21 POTENTIAL.  
FT CHAIN 22 471 TUMOR NECROSIS FACTOR RECEPTOR  
SUPERFAMILY MEMBER 1A.  
FT DOMAIN 22 210 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 211 233 POTENTIAL.  
FT DOMAIN 234 471 CYTOPLASMIC (POTENTIAL).  
FT REPEAT 43 82 TNFR-CYS 1.  
FT REPEAT 83 125 TNFR-CYS 2.  
FT REPEAT 126 166 TNFR-CYS 3.  
FT REPEAT 167 195 TNFR-CYS 4.  
FT DOMAIN 340 360 N-SMASE ACTIVATION DOMAIN (NSD).  
FT DOMAIN 372 457 DEATH.  
FT DISULFID 44 58 BY SIMILARITY.  
FT DISULFID 59 72 BY SIMILARITY.  
FT DISULFID 62 81 BY SIMILARITY.  
FT DISULFID 84 99 BY SIMILARITY.  
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FT DISULFID 105 125 BY SIMILARITY.  
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FT DISULFID 182 194 BY SIMILARITY.  
FT DISULFID 185 190 BY SIMILARITY.  
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 145 145 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 471 AA; 51367 MW; 5243EF514DFE81C4 CRC64;  
Query Match 71.7%; Score 421; DB 1; Length 471;  
Best Local Similarity 78.5%; Pred. No. 2.3e-36;  
Matches 84; Conservative 6; Mismatches 17; Indels 0; Gaps 0;  
QY 5 PQSLDQDDPATLYAVVENVPPLRWKEFVKRLGLSDHEIDRLQNGRCILREACYSMLATW 64  
Db 364 PDQLADADPATLYAVVDGVPSPRWKELVRRRLGLSHEIERLENGRHLREACYSMIAW 423  
QY 65 RRRTPREATLELLGRVLRDMDLGCLIEDIEEALCGPAALPPAPSL 111  
Db 424 RRRTPREATLELLGRVLRDMDLGCLENIEEALGGAARLASEPRLL 470

RESULT 4  
TRIA RAT STANDARD; PRT; 461 AA.  
ID P2934; Q91V30; Q91Y93;  
DT 01-AUG-1991 (Rel. 19, Created)  
DT 01-MAR-1992 (Rel. 21, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Tumor necrosis factor receptor superfamily member 1A precursor (p60)  
DE (TNF-R1) (TNF-RI) (p55).  
GN TNFRSF1A OR TNFR1 OR TNFR-1.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
SEQUENCE FROM N.A.  
RX MEDLINE=91090841; PubMed=1702293;  
RA Himmeler A., Maurer-Fogy I., Kroenke M., Scheurich P., Pfizenmaier K.,  
RA Lantz M., Olsson I., Hauptmann R., Stratowa C., Adolf G.R.;  
RT "Molecular cloning and expression of human and rat tumor necrosis  
RT factor receptor chain (p60) and its soluble derivative, tumor  
RT necrosis factor-binding protein.";  
RL DNA Cell Biol. 9:705-715(1990).  
RN [2]  
SEQUENCE FROM N.A., AND VARIANTS VAL-230 AND PRO-295.  
RC STRAIN=BB(DR)/Wor, LEW/NHsd, ACI/Seghsd, DA/BK1, F344/NHsd, and  
RC BN/SeNHsd;  
RA Furuya T., Salstrom J.L., Bina J., Hashiramoto A., Dobbins D.E.,  
RA Wilder R.L., Remmers E.F.;  
RT "Polymorphisms of the tumor necrosis factor receptor type 1 locus  
RT among autoimmune susceptible and resistant inbred rat strains.";  
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: Receptor for TNFSF2/TNF-alpha and homotrimeric  
CC TNFSF1/lymphotoxin-alpha. The adaptor molecule FADD recruits  
CC caspase-8 to the activated receptor. The resulting death-inducing  
CC signaling complex (DISC) performs caspase-8 proteolytic activation  
CC which initiates the subsequent cascade of caspases (aspartate-  
CC specific cysteine proteases) mediating apoptosis (By similarity).  
CC -!- SUBUNIT: Binding of TNF to the extracellular domain leads to  
CC homotrimerization. The aggregated death domains provide a novel  
CC molecular interface that interacts specifically with the death  
CC domain of TRADD. Various TRADD-interacting proteins such as TRAFs,  
CC RIP and possibly FADD, are recruited to the complex by their  
CC association with TRADD. This complex activates at least two  
CC distinct signaling cascades, apoptosis and NF-kappa-B signaling.  
CC Binds BAG4 (By similarity).  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.  
CC -!- SIMILARITY: Contains 1 death domain.  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
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EMBL; M63122; AAA42256.1; -.  
EMBL; AF329976; AAK53562.1; -.  
EMBL; AF329977; AAK53563.1; -.  
EMBL; AF329981; AAK53567.1; -.  
EMBL; AF329978; AAK53564.1; -.  
EMBL; AF329979; AAK53565.1; -.  
EMBL; AF329980; AAK53566.1; -.  
PIR; B36555; GQRTT1.  
HSSP; P19438; INCF.  
InterPro; IPR000488; Death.  
InterPro; IPR001368; TNFR\_c6.  
Pfam; PF00531; death; 1.  
Pfam; PF00020; TNFR\_c6; 4.

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DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 3.
DR PROSITE; PS50050; TNFR_NGFR_2; 3.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 21
FT CHAIN 22 461
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FT DOMAIN 22 211
FT TRANSMEM 212 234
FT DOMAIN 235 461
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FT REPEAT 83 125
FT REPEAT 126 166
FT REPEAT 167 196
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FT DOMAIN 363 448
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FT DISULFID 84 99
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FT DISULFID 127 143
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FT DISULFID 168 179
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FT DISULFID 185 191
FT CARBOHYD 54 54
FT CARBOHYD 151 151
FT CARBOHYD 201 201
FT VARIANT 230 230
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FT VARIANT 295 295
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FT SEQUENCE 461 AA; 50969 MW; EB23C05450FBD202 CRC64;
SQ
Query Match 65.4%; Score 384; DB 1; Length 461;
Best Local Similarity 71.6%; Pred. No. 1.6e-32;
Matches 73; Conservative 12; Mismatches 17; Indels 0; Gaps 0;
QY 1 MAHKPQSLDTPDPAITYAVVENVPLRWKEFVKRLGLSDHEIDRLQLONGRCLEAQQYSM 60
Db 351 VAAQPQRLDTADPAMLYAVVDGVPFTRWKEFMELGLSEHEIERLELQNGRCLEAHYSM 410
QY 61 LATWRRRTTPREATLELLGRVLRMDLLGCLDEDIEEALCGPA 102
Db 411 LEAWRRRTTPRHEATLDVVGRVLCMDMNLGCLNIRETLESPPA 452
RESULT 5
TRIA MOUSE STANDARD; PRT; 454 AA.
AC P25118;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 1A precursor (p60)
DE (TNF-R1) (TNF-RI) (p55).
GN TNFRSF1A OR TNFR1 OR TNFR-1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91187885; PubMed=1849278;
RA Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C.,
RA Wong G.H., Chen E.Y., Goeddel D.V.;
RT "Cloning and expression of cDNAs for two distinct murine tumor
necrosis factor receptors demonstrate one receptor is species
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RT specific.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834 (1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91246168; PubMed=1645445;
RA Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I.,
RA Copeland N.G., Jenkins N.A., Smith C.A.;
RT "Molecular cloning and expression of the type 1 and type 2 murine
receptors for tumor necrosis factor.";
RL Mol. Cell. Biol. 11:3020-3026 (1991).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=91285014; PubMed=1647956;
RA Barrett K., Taylor-Fishwick D.A., Cope A.P., Kissonerghis A.M.,
RA Gray P.W., Feldmann M., Foxwell B.M.J.;
RT "Cloning, expression and cross-linking analysis of the murine p55
tumor necrosis factor receptor.";
RL Eur. J. Immunol. 21:1649-1656 (1991).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=92039815; PubMed=1657766;
RA Rothe J.G., Brockhaus M., Gentz R., Lesslauer W.;
RT "Molecular cloning and expression of the mouse Tnf receptor type b.";
RL Immunogenetics 34:338-340 (1991).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=94245292; PubMed=8188324;
RA Bebo B.F., Linthicum D.S.;
RT "Nucleotide sequence of the TNF type I receptor from a mouse
endothelioma cell line.";
RL Immunogenetics 39:450-451 (1994).
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE=93156721; PubMed=8381516;
RA Rothe J., Bluethmann H., Gentz R., Lesslauer W., Steinmetz M.;
RT "Genomic organization and promoter function of the murine tumor
necrosis factor receptor beta gene.";
RL Mol. Immunol. 30:165-175 (1993).
RN [7]
RP SEQUENCE FROM N.A.
RX STRAIN=C3H/He; TISSUE=Mesenchyme;
MEDLINE=22388257; PubMed=12477932;
RA Krausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -!- FUNCTION: Receptor for TNFSF2/TNF-alpha and homotrimeric
TNFSF1/lymphotoxin-alpha. The adaptor molecule FADD recruits
caspase-8 to the activated receptor. The resulting death-inducing
signaling complex (DISC) performs caspase-8 proteolytic activation
which initiates the subsequent cascade of caspases (aspartate-
specific cysteine proteases) mediating apoptosis (By similarity).
CC -!- SUBUNIT: Binding of TNF to the extracellular domain leads to
homotrimerization. The aggregated death domains provide a novel
molecular interface that interacts specifically with the death
domain of TRADD. Various TRADD-interacting proteins such as TRAFs,
```











RP SEQUENCE FROM N.A.  
RA Sycamore N.;  
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE OF 300-671 FROM N.A.  
RC TISSUE=Leukemic T-cell;  
RX MEDLINE=95277838; PubMed=7538908;  
RA Stanger B.Z., Leder P., Lee T.-H., Kim E., Seed B.;  
RT "RIP: a novel protein containing a death domain that interacts with  
RT Fas/APO-1 (CD95) in yeast and causes cell death.";  
RL Cell 81:513-523(1995).  
RN [5]  
RP CLEAVAGE BY CASPASE-8, AND MUTAGENESIS OF ASP-324.  
RX MEDLINE=99452794; PubMed=10521396;  
RA Lin Y., Devin A., Rodriguez Y., Liu Z.-G.;  
RT "Cleavage of the death domain kinase RIP by caspase-8 prompts  
RT TNF-induced apoptosis";  
RL Genes Dev. 13:2514-2526(1999).  
RN [6]  
RP INTERACTION WITH RIPK3.  
RX MEDLINE=99287880; PubMed=10358032;  
RA Sun X., Lee J., Navas T., Baldwin D.T., Stewart T.A., Dixit V.M.;  
RT "RIP3, a novel apoptosis-inducing kinase.";  
RL J. Biol. Chem. 274:16871-16875(1999).  
RN [7]  
RP INTERACTION WITH BNLf1.  
RX MEDLINE=99340272; PubMed=10409763;  
RA Izumi K.M., Cahir McFarland E., Ting A.T., Riley E.A., Seed B.,  
RA Kieff E.D.;  
RT "The Epstein-Barr virus oncoprotein latent membrane protein 1 engages  
RT the tumor necrosis factor receptor-associated proteins TRADD and  
RT receptor-interacting protein (RIP) but does not induce apoptosis or  
RT require RIP for NF-kappaB activation.";  
RL Mol. Cell. Biol. 19:5759-5767(1999).  
RN [8]  
RP INTERACTION WITH IKKb.  
RX MEDLINE=99128359; PubMed=9927690;  
RA Li Y., Kang J., Friedman J., Tarassishin L., Ye J., Kovalenko A.,  
RA Wallach D., Horwitz M.S.;  
RT "Identification of a cell protein (FIP-3) as a modulator of NF-kappaB  
RT activity and as a target of an adenovirus inhibitor of tumor necrosis  
RT factor alpha-induced apoptosis.";  
RL Proc. Natl. Acad. Sci. U.S.A. 96:1042-1047(1999).  
RN [9]  
RP INTERACTION WITH EGFR.  
RX MEDLINE=21153697; PubMed=11116146;  
RA Habib A.A., Chatterjee S., Park S.-K., Ratan R.R., Lefebvre S.,  
RA Vartanian T.;  
RT "The epidermal growth factor receptor engages receptor interacting  
RT protein and nuclear factor-kappa B (NF-kappa B)-inducing kinase to  
RT activate NF-kappa B. Identification of a novel receptor-tyrosine  
RT kinase signalosome.";  
RL J. Biol. Chem. 276:8865-8874(2001).  
RN [10]  
RP INTERACTION WITH UBCE7IP1.  
RX MEDLINE=21975204; PubMed=11854271;  
RA Chen D., Li X., Zhai Z., Shu H.-B.;  
RT "A novel zinc finger protein interacts with receptor-interacting  
RT protein (RIP) and inhibits tumor necrosis factor (TNF)- and  
RT IL1-induced NF-kappa B activation.";  
RL J. Biol. Chem. 277:15985-15991(2002).  
CC -!- FUNCTION: Promotes apoptosis and activation of NF-kappa-B.  
CC Required for TNFRSF1A mediated activation of NF-kappa-B.  
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
CC -!- SUBUNIT: Binds to the death domain of TNFRSF6 and TRADD. Is  
CC recruited by TRADD to TNFRSF1A in a TNF-dependent process. Binds  
CC RIPK3, UBCE7IP1, EGFR, IKKb, TRAF1, TRAF2 and TRAF3. Interacts  
CC with BNLf1.  
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -!- PTM: Proteolytically cleaved by caspase-8 during TNF-induced  
CC apoptosis. Cleavage abolishes NF-kappa-B activation and enhances  
CC pro-apoptotic signaling through the TRADD-FADD interaction.  
CC -!- PTM: Autophosphorylated on serine and threonine residues.

CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.  
CC -!- SIMILARITY: Contains 1 death domain.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; U50062; AAC32232.1; -.  
DR EMBL; AL031963; CAD70625.1; -.  
DR EMBL; U25994; AAC50137.1; -.  
DR PIR; T09479; T09479.  
DR HSSP; P08631; IAD5.  
DR Genew; HGNC:10019; RIPK1.  
DR MIM; 603453; -.  
DR GO; GO:0004674; F:protein serine/threonine kinase activity; TAS.  
DR GO; GO:0006915; P:apoptosis; TAS.  
DR GO; GO:0007165; P:signal transduction; TAS.  
DR InterPro; IPR000488; Death.  
DR InterPro; IPR000719; Prot\_kinase.  
DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
DR InterPro; IPR001245; Tyr\_pkinase.  
DR Pfam; PF00531; death; 1.  
DR Pfam; PF00069; pkinase; 1.  
DR PRINTS; PR00109; TYRKINASE.  
DR ProDom; PD000001; Prot\_kinase; 1.  
DR SMART; SM00005; DEATH; 1.  
DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE; PS50017; DEATH\_DOMAIN; 1.  
KW Transferase; Serine/threonine-protein kinase; ATP-binding;  
KW Phosphorylation; Apoptosis.  
FT DOMAIN 17 289 PROTEIN KINASE.  
FT NP\_BIND 23 31 ATP (BY SIMILARITY).  
FT BINDING 49 49 ATP (BY SIMILARITY).  
FT ACT\_SITE 138 138 BY SIMILARITY.  
FT DOMAIN 411 414 DEATH.  
FT SITE 324 325 POLY-ARG.  
FT MUTAGEN 45 45 CLEAVAGE (BY CASPASE-8).  
FT MUTAGEN 324 324 K->A: ABOLISHES KINASE ACTIVITY.  
FT CONFLICT 438 438 D->K: ABOLISHES CLEAVAGE BY CASPASE-8.  
FT CONFLICT 514 514 V -> A (IN REF. 3).  
FT CONFLICT 514 514 T -> S (IN REF. 4).  
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Query Match 15.1%; Score 88.5; DB 1; Length 671;  
Best local Similarity 27.0%; Pred. No. 0.16;  
Matches 27; Conservative 18; Mismatches 36; Indels 19; Gaps 4;  
  
QY 11 DDPATLYAVV-----ENVPLR-----WKEFVKRLGLSDHEIDRLQLNGR-CLR 54  
Db 566 EEPAAKYQAFDNTTSLTDKHLDPRENLGKHWKNCARKLGFTQSQIDEIDHYERDGLK 625  
QY 55 EAQYSMLATWRRRTPRREATLELLGRVLRD---MDLLGCL 91  
Db 626 EKVIQMLQKWMVREGIKGATVGKLAQALHQCSRIDLLSSL 665  
  
RESULT 9  
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AC Q60855; Q8CD90;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Receptor-interacting serine/threonine protein kinase 2 (EC 2.7.1.37)  
DE (Serine/threonine protein kinase RIP) (Cell death protein RIP)  
DE (Receptor interacting protein).  
GN RIPK1 OR RIP OR RINP.  
OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6 X CBA; TISSUE=Thymus;  
RX MEDLINE=22354683; PubMed=12466851;  
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
RA Nikaïdo I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,  
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,  
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,  
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,  
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
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RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,  
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,  
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,  
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,  
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
RA Verardo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,  
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,  
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,  
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
RA Birney E., Hayashizaki Y.;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs.";  
RL Nature 420:563-573 (2002).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6; TISSUE=Brain, and Liver;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length  
RT human and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
CC -!- FUNCTION: Promotes apoptosis and activation of NF-kappa-B.  
CC Required for TNFRSF1A mediated activation of NF-kappa-B.  
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
CC -!- SUBUNIT: Binds to the death domain of TNFRSF6 and TRADD. Is  
CC recruited by TRADD to TNFRSF1A in a TNF-dependent process. Binds

CC RIPK3, UBCE7IP1, EGFR, IKBKG, TRAF1, TRAF2 and TRAF3. Interacts  
CC with BNLF1 (By similarity).  
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -!- TISSUE SPECIFICITY: Found at low levels in all tissues.  
CC -!- INDUCTION: In Concanavalin A-treated splenocytes.  
CC -!- PTM: Proteolytically cleaved by caspase-8 during TNF-induced  
CC apoptosis. Cleavage abolishes NF-kappa-B activation and enhances  
CC pro-apoptotic signaling through the TRADD-FADD interaction (By  
CC similarity).  
CC -!- PTM: Autophosphorylated on serine and threonine residues (By  
CC similarity).  
CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.  
CC -!- SIMILARITY: Contains 1 death domain.  
CC -----  
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CC -----  
DR EMBL; U25995; AAB60487.1; -.  
DR EMBL; AK030959; BAC27194.1; -.  
DR EMBL; BC050905; AAH50905.1; ALT\_INIT.  
DR EMBL; BC054542; AAH54542.1; -.  
DR EMBL; BC058162; AAH58162.1; -.  
DR PIR; I49299; I49299.  
DR HSSP; P25445; IDDF.  
DR MGD; MGI:108212; Ripk1.  
DR InterPro; IPR000488; Death.  
DR InterPro; IPR000719; Prot\_kinase.  
DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
DR InterPro; IPR001245; Tyr\_pkinase.  
DR Pfam; PF00531; death; 1.  
DR Pfam; PF00069; pkinase; 1.  
DR PRINTS; PR00109; TYRKINASE.  
DR ProDom; PD000001; Prot\_kinase; 1.  
DR SMART; SM00005; DEATH; 1.  
DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE; PS50017; DEATH\_DOMAIN; 1.  
KW Transferase; Serine/threonine-protein kinase; ATP-binding;  
KW Apoptosis.  
KW DOMAIN 17 290 PROTEIN\_KINASE.  
FT NP\_BIND 23 31 ATP (BY SIMILARITY).  
FT BINDING 46 46 ATP (BY SIMILARITY).  
FT ACT\_SITE 138 138 BY SIMILARITY.  
FT DOMAIN 568 654 DEATH.  
FT VARIANT 473 473 T -> I.  
FT CONFLICT 66 66 M -> K (IN REF. 2).  
SQ SEQUENCE 656 AA; 74854 MW; ABB350B523879933 CRC64;  
  
Query Match 14.8%; Score 87; DB 1; Length 656;  
Best Local Similarity 30.9%; Pred. No. 0.23;  
Matches 25; Conservative 15; Mismatches 31; Indels 10; Gaps 3;  
  
QY 21 ENVPLR-----WKEFVKRLGLSDHEIDRLQNGR-CLREAYSMLATWRRRTPRREA 73  
Db 570 EHLNPIRENIGRWKNCARKLGFTESQIDHIDHYERDGLKXKVVQMLQKWLMEGTGKA 629  
QY 74 TLELLGRVLRD---MDLLGCL 91  
Db 630 TVGKLAQALHQCCRIDLNLHL 650  
  
RESULT 10  
ANK1\_MOUSE  
ID ANK1\_MOUSE STANDARD; PRT; 1862 AA.  
AC Q02357;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)

Ankyrin 1 (Erythrocyte ankyrin).

ANK1 OR ANK-1.  
Mus musculus (Mouse).  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
NCBI\_TaxID=10090;  
[1]  
SEQUENCE FROM N.A.  
TISSUE=Erythrocyte;  
MEDLINE=92345717; PubMed=1386265;  
White R.A., Birkenmeier C.S., Peters L.L., Barker J.E., Lux S.E.;  
"Murine erythrocyte ankyrin cDNA: highly conserved regions of the  
regulatory domain."  
Mamm. Genome 3:281-285(1992).  
-!- FUNCTION: Attach integral membrane proteins to cytoskeletal  
elements; bind to the erythrocyte membrane protein band 4.2, to  
Na-K ATPase, to the lymphocyte membrane protein GP85, and to the  
cytoskeletal proteins fodrin, tubulin, vimentin and desmin.  
Erythrocyte ankyrins also link spectrin (beta chain) to the  
cytoplasmic domain of the erythrocytes anion exchange protein;  
they retain most or all of these binding functions.  
-!- SUBCELLULAR LOCATION: CYTOPLASMIC SURFACE OF ERYTHROCYTIC  
PLASMA MEMBRANE.  
-!- PTM: Regulated by phosphorylation (By similarity).  
-!- PTM: Acylated by palmitic acid group(s) (By similarity).  
-!- SIMILARITY: Contains 23 ANK repeats.  
-!- SIMILARITY: Contains 1 death domain.  
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EMBL; M84756; AAA37236.1; -.  
PIR; I49502; I49502.  
HSSP; Q00420; IAWC.  
MGD; MGI:88024; Ank1.  
InterPro; IPR002110; ANK.  
InterPro; IPR000488; Death.  
InterPro; IPR000906; ZU5.  
Pfam; PF00023; ank; 24.  
Pfam; PF00531; death; 1.  
Pfam; PF00791; ZU5; 1.  
PRINTS; PR01415; ANKYRIN.  
SMART; SM00248; ANK; 22.  
SMART; SM00005; DEATH; 1.  
SMART; SM00218; ZU5; 1.  
PROSITE; PS50088; ANK\_REPEAT; 20.  
PROSITE; PS50297; ANK\_REPEAT\_REGION; 1.  
PROSITE; PS50017; DEATH\_DOMAIN; 1.  
Cytoskeleton; Repeat; ANK repeat; Phosphorylation; Lipoprotein.  
DOMAIN 1 827 89 kDa DOMAIN (ANION EXCHANGE PROTEIN  
BINDING DOMAIN).  
DOMAIN 828 1386 62 kDa DOMAIN (SPECTRIN BINDING  
DOMAIN).  
DOMAIN 1387 1862 55 kDa REGULATORY DOMAIN (REGULATES  
THE BINDING OF ANKYRIN TO SPECTRIN  
AND THE BAND 3 PROTEIN).  
REPEAT 40 69  
REPEAT 73 102  
REPEAT 106 135  
REPEAT 139 168  
REPEAT 170 197  
REPEAT 201 230  
REPEAT 234 263  
REPEAT 267 296  
REPEAT 300 329  
REPEAT 333 362  
REPEAT 366 395  
REPEAT 399 428

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RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880 (2002).
CC -!- FUNCTION: MAY PLAY A ROLE IN MEDIATING THE HEAT SHOCK RESPONSE
CC OF SOME HSP70 GENES (BY SIMILARITY).
CC -!- SUBUNIT: PART OF A LARGER COMPLEX THAT INCLUDES HSP70, HSP90, AND
CC IMMUNOPHILINS (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Contains 9 TPR repeats.
CC -----
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CC -----
DR EMBL; D85197; BAA22619.1; -.
DR EMBL; AL049498; CAB39910.1; -.
DR PIR; T41531; T41531.
DR PIR; T51996; T51996.
DR HSSP; P53041; 1A17.
DR GeneDB_Spombe; SPCC645.14c; -.
DR InterPro; IPR006636; STI1.
DR InterPro; IPR008941; TPR-like.
DR InterPro; IPR001440; TPR.
DR Pfam; PF00515; TPR; 8.
DR SMART; SM00727; STI1; 2.
DR SMART; SM00028; TPR; 8.
KW Heat shock; TPR repeat; Repeat.
FT REPEAT 2 35 TPR 1.
FT REPEAT 37 69 TPR 2.
FT REPEAT 70 103 TPR 3.
FT REPEAT 265 298 TPR 4.
FT REPEAT 299 331 TPR 5.
FT REPEAT 339 372 TPR 6.
FT REPEAT 399 432 TPR 7.
FT REPEAT 434 466 TPR 8.
FT REPEAT 467 500 TPR 9.
FT CONFLICT 28 28 A -> T (IN REF. 1).
SQ SEQUENCE 591 AA; 65544 MW; D218FCCD5884B4AA CRC64;

Query Match 13.2%; Score 77.5; DB 1; Length 591;
Best Local Similarity 32.4%; Pred. No. 2;
Matches 24; Conservative 14; Mismatches 25; Indels 11; Gaps 3;

QY 41 EIDRLQLQGRCLRAQ-----YSMLATWRRTPRREATLELLGRVLRDMDLLGCLD- 93
Db 495 EVDRREPNTGKNLREIESQLSKCMSASQR----QNETEEETMARIQDPVLGILQDP 550
QY 94 IEEALCGPAALPPA 107
Db 551 AMQAILGQARENPA 564

RESULT 12
ANK3_HUMAN
ID ANK3_HUMAN STANDARD; PRT; 4377 AA.
AC Q12955;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Ankyrin 3 (ANK-3) (Ankyrin G).
GN ANK3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
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RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain stem;
RX MEDLINE=95138209; PubMed=7836469;
RA Kordeli E., Lambert S., Bennett V.;
RT "AnkyrinG. A new ankyrin gene with neural-specific isoforms localized
RT at the axonal initial segment and node of Ranvier.";
RL J. Biol. Chem. 270:2352-2359(1995).
CC -!- FUNCTION: Membrane-cytoskeleton linker. The neural-specific
CC isoforms may participate in the maintenance/targeting of ion
CC channels and cell adhesion molecules at the nodes of Ranvier and
CC axonal initial segments.
CC -!- SUBUNIT: Neural-specific isoforms may be a constituent of a
CC neurofascin/NRCAM/ankyrin G complex.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=1;
CC Comment=A number of isoforms are produced;
CC Name=1; Synonyms=480-kDa isoform;
CC IsoId=Q12955-1; Sequence=Displayed;
CC -!- TISSUE SPECIFICITY: Expressed in brain and other tissues. Isoform
CC 1 is neural-specific.
CC -!- SIMILARITY: Contains 23 ANK repeats.
CC -!- SIMILARITY: Contains 1 death domain.
CC -----
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CC -----
DR EMBL; U13616; AAA64834.1; -.
DR PIR; A55575; A55575.
DR HSSP; P55273; 1BI8.
DR Genew; HGNC:494; ANK3.
DR MIM; 600465; -.
DR GO; GO:0006605; P:protein targeting; NAS.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR000488; Death.
DR InterPro; IPR000906; ZU5.
DR Pfam; PF00023; ank; 24.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00791; ZU5; 1.
DR PRINTS; PR01415; ANKYRIN.
DR SMART; SM00248; ANK; 21.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00218; ZU5; 1.
DR PROSITE; PS50088; ANK_REPEAT; 21.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
KW Cytoskeleton; Alternative splicing; Repeat; ANK repeat.
FT REPEAT 73 102 ANK 1.
FT REPEAT 106 135 ANK 2.
FT REPEAT 139 168 ANK 3.
FT REPEAT 172 201 ANK 4.
FT REPEAT 203 230 ANK 5.
FT REPEAT 234 263 ANK 6.
FT REPEAT 267 296 ANK 7.
FT REPEAT 300 329 ANK 8.
FT REPEAT 333 362 ANK 9.
FT REPEAT 366 395 ANK 10.
FT REPEAT 399 428 ANK 11.
FT REPEAT 432 461 ANK 12.
FT REPEAT 465 494 ANK 13.
FT REPEAT 498 527 ANK 14.
FT REPEAT 531 560 ANK 15.
FT REPEAT 564 593 ANK 16.
FT REPEAT 597 626 ANK 17.
FT REPEAT 630 659 ANK 18.
FT REPEAT 663 692 ANK 19.
FT REPEAT 696 725 ANK 20.
FT REPEAT 729 758 ANK 21.
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FT	VARSPLIC	1512	1873	Missing (in isoform 2). /FTid=VSP_000264.
FT	VARSPLIC	1874	1874	H -> D (in isoform 2). /FTid=VSP_000265.
FT	VARSPLIC	1849	1880	TVEGPLEDPSELEVDIDYFMKHSKDHTSTPNP -> ELRGS GLQPDLEGRKGAQIVKRASLKRKQ (in isoform 3).
FT	VARIANT	20	20	/FTid=VSP_000266. R -> T.
FT	VARIANT	462	462	/FTid=VAR_000595. V -> I (in HS).
FT	VARIANT	618	618	/FTid=VAR_000596. R -> H (in Brueggen).
FT	VARIANT	749	749	/FTid=VAR_000597. V -> A.
FT	VARIANT	844	844	/FTid=VAR_000598. D -> E.
FT	VARIANT	1285	1285	/FTid=VAR_000599. E -> D.
FT	VARIANT	1391	1391	/FTid=VAR_000601. S -> T.
FT	VARIANT	1591	1591	/FTid=VAR_000600. D -> N (in Duesseldorf).
FT	VARIANT	1698	1698	/FTid=VAR_000602. R -> D.
FT	CONFLICT	229	229	/FTid=VAR_000603. A -> S (IN REF. 2).
FT	CONFLICT	1545	1545	V -> I (IN REF. 2).
SQ	SEQUENCE	1880 AA;	206145 MW;	1C5F5E7EFD1CD428 CRC64;
Query Match 13.1%; Score 77; DB 1; Length 1880;				
Best Local Similarity 28.9%; Pred. No. 8.1;				
Matches 24; Conservative 15; Mismatches 42; Indels 2; Gaps 2;				
QY	5	PGSLDTPPATL-YAVVENVPLRWKEFVKRLGLSDHEIDRLQNGRCLEACYSMLAT	63	
Db	1393	PGSLSGTEQAEMKMAVISEHGLSWAELARELQFVEDINRIRVENPNSLLEQSVALLNL	1452	
QY	64	WRRTPREATLELLGRVLRDMD	86	
Db	1453	WVIR-EGQNANMENLYTALQSID	1474	
RESULT 14				
T10B_HUMAN				
ID	T10B_HUMAN	STANDARD;	PRT;	440 AA.
AC	O14763;	O14720;	O15508;	O15517; O15531; Q9BVE0;
DT	16-OCT-2001	(Rel. 40, Created)		
DT	16-OCT-2001	(Rel. 40, Last sequence update)		
DT	10-OCT-2003	(Rel. 42, Last annotation update)		
DE	Tumor necrosis factor receptor superfamily member 10B precursor (Death			
DE	receptor 5) (TNF-related apoptosis-inducing ligand receptor 2) (TRAIL			
DE	receptor-2) (TRAIL-R2).			
GN	TNFRSF10B OR DR5 OR TRAILR2 OR TRICK2 OR KILLER OR ZTNFR9.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORM LONG), AND SEQUENCE OF N-TERMINUS.			
RC	TISSUE=Foreskin fibroblast;			
RX	MEDLINE=97459925; PubMed=9311998;			
RA	Walczak H., Degli-Esposti M.A., Johnson R.S., Smolak P.J., Waugh J.Y.,			
RA	Boiani N., Timour M.S., Gerhart M.J., Schooley K.A., Smith C.A.,			
RA	Goodwin R.G., Rauch C.T.;			
RT	"TRAIL-R2: a novel apoptosis-mediating receptor for TRAIL.";			
RL	EMBO J. 16:5386-5397(1997).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT), ALTERNATIVE			
RP	SPLICING, AND VARIANTS LEU-32 AND VAL-67.			
RX	MEDLINE=97431692; PubMed=9285725;			
RA	Screaton G.R., Mongkolsapaya J., Xu X.-N., Cowper A.E.,			
RA	McMichael A.J., Bell J.I.;			

RT	"TRICK2, a new alternatively spliced receptor that transduces the			
RT	cytotoxic signal from TRAIL.";			
RL	Curr. Biol. 7:693-696(1997).			
RN	[3]			
RP	SEQUENCE FROM N.A. (ISOFORM LONG), CHARACTERIZATION, AND VARIANTS			
RP	LEU-32 AND VAL-67.			
RC	TISSUE=Liver, and Spleen;			
RX	MEDLINE=98039016; PubMed=9373179;			
RA	Schneider P., Bodmer J.-L., Thome M., Hofmann K., Holler N.,			
RA	Tschopp J.;			
RT	"Characterization of two receptors for TRAIL.";			
RL	FEBS Lett. 416:329-334(1997).			
RN	[4]			
RP	SEQUENCE FROM N.A. (ISOFORM SHORT).			
RC	TISSUE=Ovary;			
RX	MEDLINE=97467719; PubMed=9326928;			
RA	Wu G.S., Burns T.F., McDonald E.R. III, Jiang W., Meng R.,			
RA	Krantz I.D., Kao G., Gan D.D., Zhou J.Y., Muschel R., Hamilton S.R.,			
RA	Spinner N.B., Markowitz S., Wu G., el-Deiry W.S.;			
RT	"KILLER/DR5 is a DNA damage-inducible p53-regulated death receptor			
RT	gene.";			
RL	Nat. Genet. 17:141-143(1997).			
RN	[5]			
RP	SEQUENCE FROM N.A. (ISOFORM SHORT).			
RX	MEDLINE=97390508; PubMed=9242610;			
RA	Pan G., Ni J., Wei Y.-F., Yu G.-I., Gentz R., Dixit V.M.;			
RT	"An antagonist decoy receptor and a death domain-containing receptor			
RT	for TRAIL.";			
RL	Science 277:815-818(1997).			
RN	[6]			
RP	SEQUENCE FROM N.A. (ISOFORM SHORT), AND VARIANTS LEU-32 AND VAL-67.			
RX	MEDLINE=97467318; PubMed=9325248;			
RA	MacFarlane M., Ahmad M., Srinivasula S.M., Fernandes-Alnemri T.,			
RA	Cohen G.M., Alnemri E.S.;			
RT	"Identification and molecular cloning of two novel receptors for the			
RT	cytotoxic ligand TRAIL.";			
RL	J. Biol. Chem. 272:25417-25420(1997).			
RN	[7]			
RP	SEQUENCE FROM N.A. (ISOFORM SHORT), AND VARIANTS LEU-32 AND VAL-67.			
RX	MEDLINE=98090092; PubMed=9430227;			
RA	Chaudhary P.M., Eby M., Jasmin A., Bookwalter A., Murray J., Hood L.;			
RT	"Death receptor 5, a new member of the TNFR family, and DR4 induce			
RT	FADD-dependent apoptosis and activate the NF-kappaB pathway.";			
RL	Immunity 7:821-830(1997).			
RN	[8]			
RP	SEQUENCE FROM N.A. (ISOFORM SHORT), AND VARIANT LEU-32.			
RX	MEDLINE=97390509; PubMed=9242611;			
RA	Sheridan J.P., Marsters S.A., Pitti R.M., Gurney A., Skubatch M.,			
RA	Baldwin D., Ramakrishnan L., Gray C.L., Baker K., Wood W.I.,			
RA	Goddard A.D., Godowski P., Ashkenazi A.;			
RT	"Control of TRAIL-induced apoptosis by a family of signaling and decoy			
RT	receptors.";			
RL	Science 277:818-821(1997).			
RN	[9]			
RP	SEQUENCE FROM N.A. (ISOFORM LONG), AND VARIANTS LEU-32 AND VAL-67.			
RA	Arai T., Akiyama Y., Okabe S., Saito K., Iwai T., Yuasa Y.;			
RT	"Genomic structure and mutation analyses of the DR5/TRAIL receptor 2			
RT	gene in colorectal carcinoma.";			
RL	Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.			
RN	[10]			
RP	SEQUENCE FROM N.A. (ISOFORM SHORT).			
RA	Cao X., Zhang W., Wan T.;			
RL	Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.			
RN	[11]			
RP	SEQUENCE FROM N.A. (ISOFORM SHORT), AND VARIANTS LEU-32 AND VAL-67.			
RA	Farrah T., Vu T., Gilbert T., Gross J., O'Hara P.;			
RT	"Homo sapiens homolog of tumor necrosis factor receptor.";			
RL	Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.			
RN	[12]			
RP	SEQUENCE FROM N.A. (ISOFORM LONG), AND VARIANT LEU-32.			
RC	TISSUE=Cervix;			
RX	MEDLINE=22388257; PubMed=12477932;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Touchman J.W., Green E.D., Dickson M.C.,  
RA Blakesley R.W., Grimwood J., Schmutz J., Myers R.M.,  
RA Rodriguez A.C., Grimwood J., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Marra M.A.;  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length  
RT human and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [13]  
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 54-183.  
RX MEDLINE=20017054; PubMed=10549288;  
RA Hymowitz S.G., Christinger H.W., Fuh G., Ultsch M., O'Connell M.,  
RA Kelley R.F., Ashkenazi A., de Vos A.M.;  
RT "Triggering cell death: the crystal structure of Apo2L/TRAIL in a  
RT complex with death receptor 5";  
RL Mol. Cell 4:563-571 (1999).  
RN [14]  
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 69-184.  
RX PubMed=10542098;  
RA Mongkolsapaya J., Grimes J.M., Chen N., Xu X.-N., Stuart D.I.,  
RA Jones E.Y., Screaton G.R.;  
RT "Structure of the TRAIL-DR5 complex reveals mechanisms conferring  
RT specificity in apoptotic initiation.";  
RL Nat. Struct. Biol. 6:1048-1053 (1999).  
CC -!- FUNCTION: Receptor for the cytotoxic ligand TNFSF10/TRAIL. The  
CC adaptor molecule FADD recruits caspase-8 to the activated  
CC receptor. The resulting death-inducing signaling complex (DISC)  
CC performs caspase-8 proteolytic activation which initiates the  
CC subsequent cascade of caspases (aspartate-specific cysteine  
CC proteases) mediating apoptosis. Promotes the activation of NF-  
CC kappaB.  
CC -!- SUBUNIT: Homotrimer. Can interact with TRADD and RIP.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=Long; Synonyms=TRICK2B;  
CC IsoId=O14763-1; Sequence=Displayed;  
CC Name=Short; Synonyms=TRICK2A;  
CC IsoId=O14763-2; Sequence=VSP\_006490;  
CC -!- TISSUE SPECIFICITY: Widely expressed in adult and fetal tissues;  
CC very highly expressed in tumor cell lines such as HeLa S3, K562,  
CC HL-60, SW480, A549 and G361; highly expressed in heart, peripheral  
CC blood lymphocytes, liver, pancreas, spleen, thymus, prostate,  
CC ovary, uterus, placenta, testis, esophagus, stomach and throughout  
CC the intestinal tract; not detectable in brain.  
CC -!- INDUCTION: TNFRSF10B is regulated by the tumor suppressor p53.  
CC -!- DISEASE: Defects in TNFRSF10B may be a cause of squamous cell  
CC carcinoma of the head and neck (HNSCC) [MIM:601400].  
CC -!- SIMILARITY: Contains 3 TNFR-Cys repeats.  
CC -!- SIMILARITY: Contains 1 death domain.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; AF016849; AAC51778.1; --  
DR EMBL; AF018657; AAB70577.1; --  
DR EMBL; AF018658; AAB70578.1; --

DR EMBL; AF016266; AAB81180.1; --  
DR EMBL; AF022386; AAB71949.1; --  
DR EMBL; AF012628; AAB67109.1; --  
DR EMBL; AF020501; AAB71412.1; --  
DR EMBL; AF016268; AAC01565.1; --  
DR EMBL; AF012535; AAB67103.1; --  
DR EMBL; AB014718; BAA33723.1; --  
DR EMBL; AB014710; BAA33723.1; JOINED.  
DR EMBL; AB014711; BAA33723.1; JOINED.  
DR EMBL; AB014712; BAA33723.1; JOINED.  
DR EMBL; AB014713; BAA33723.1; JOINED.  
DR EMBL; AB014714; BAA33723.1; JOINED.  
DR EMBL; AB014715; BAA33723.1; JOINED.  
DR EMBL; AB014716; BAA33723.1; JOINED.  
DR EMBL; AB014717; BAA33723.1; JOINED.  
DR EMBL; AF153687; AAF75587.1; --  
DR EMBL; AF192548; AAF07175.1; --  
DR EMBL; BC001281; AAH01281.1; --  
DR PDB; 1D0G; 22-OCT-99.  
DR PDB; 1D4V; 01-NOV-99.  
DR PDB; HGNC:11905; TNFRSF10B.  
DR MIM; 603612; --  
DR MIM; 601400; --  
DR GO; GO:0016021; C:integral to membrane; IC.  
DR GO; GO:0016506; F:apoptosis activator activity; NAS.  
DR GO; GO:0008656; F:caspase activator activity; NAS.  
  
Query Match 12.5%; Score 73.5; DB 1; Length 440;  
Best Local Similarity 30.7%; Pred. No. 3.7;  
Matches 27; Conservative 11; Mismatches 33; Indels 17; Gaps 3;  
  
QY 11 DDPATLYAVVENVPPLRWKEFVKRLGLSDHETDRLELQNGRCLREAQYSMLATWRRRTPR 70  
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :||| :|  
343 DDFADL-----VPFDSWEPLMRKLGMDNET-KVAKAEAAAGHRDITLYTMLIKVWVNT-- 393  
  
QY 71 REATLELLGRVLRDMDLLGCLIEDIEEAL 98  
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :||| :|  
394 -----GRDASVHTLLDALETIGERL 413  
  
RESULT 15  
SYQ\_XYLEFA  
ID SYQ\_XYLEFA STANDARD; PRT; 580 AA.  
AC Q9PDP1;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Glutaminyl-tRNA synthetase (EC 6.1.1.18) (Glutamine--tRNA ligase)  
DE (GlnRS).  
GN GLNS OR XF1338.  
OS Xylella fastidiosa.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;  
OC Xanthomonadaceae; Xylella.  
OX NCBI\_TaxID=2371;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=9a5C;  
RX MEDLINE=20365717; PubMed=10910347;  
RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,  
RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,  
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,  
RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,  
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,  
RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorri H.,  
RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,  
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,  
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,  
RA Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,  
RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,  
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,  
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,  
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,  
RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.;



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OM protein - protein search, using sw model

Run on: June 1, 2004, 14:35:21 ; Search time 33.5329 Seconds  
(without alignments)  
1053.831 Million cell updates/sec

Title: US-09-854-906-1  
Perfect score: 587  
Sequence: 1 MAHKPQSLDTDDPATLYAVV.....DIEEALCGPAALPPAPSLLR 112

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : SPTREMBL 25:\*
- 1: sp\_archea.\*
  - 2: sp\_bacteria.\*
  - 3: sp\_fungi.\*
  - 4: sp\_human.\*
  - 5: sp\_invertebrate.\*
  - 6: sp\_mammal.\*
  - 7: sp\_mhc.\*
  - 8: sp\_organelle.\*
  - 9: sp\_phage.\*
  - 10: sp\_plant.\*
  - 11: sp\_rodent.\*
  - 12: sp\_virus.\*
  - 13: sp\_vertebrate.\*
  - 14: sp\_unclassified.\*
  - 15: sp\_rvirus.\*
  - 16: sp\_bacteriap.\*
  - 17: sp\_archeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	474.5	80.8	446	6	Q95ND3	Q95nd3 felis silve
2	155	26.4	387	11	Q8VD70	Q8vd70 mus musculu
3	149	25.4	413	11	Q99MM1	Q99mm1 mus musculu
4	83	14.1	410	13	Q7T3M8	Q7t3m8 gallus gall
5	83	14.1	1848	11	Q61302	Q61302 mus musculu
6	82.5	14.1	365	12	Q81645	Q81645 hepatitis c
7	82.5	14.1	3011	12	Q913D4	Q913d4 hepatitis c
8	82	14.0	163	17	Q9YBB1	Q9ybb1 aeropyrum p
9	81.5	13.9	364	12	Q68797	Q68797 hepatitis c
10	81.5	13.9	365	12	Q81652	Q81652 hepatitis c
11	81.5	13.9	634	5	Q8STZ1	Q8stz1 encephalito
12	81.5	13.9	3011	12	Q81754	Q81754 hepatitis c
13	81.5	13.9	3022	12	Q68798	Q68798 hepatitis c
14	80.5	13.7	368	13	O57408	O57408 meleagris g
15	80	13.6	273	5	Q9V8H5	Q9v8h5 drosophila
16	79.5	13.5	634	5	Q8ST44	Q8st44 encephalito

17	79	13.5	143	11	O70510	O70510 rattus norv
18	79	13.5	960	11	Q8VDA0	Q8vda0 rattus norv
19	78	13.3	626	16	Q9KYP5	Q9kyp5 streptomyce
20	77.5	13.2	314	6	Q861W6	Q861w6 felis silve
21	77.5	13.2	838	11	Q9QXH1	Q9qxh1 mus musculu
22	77.5	13.2	1093	11	Q8CBN3	Q8cbn3 mus musculu
23	77.5	13.2	1726	11	Q8VC68	Q8vc68 mus musculu
24	77.5	13.2	1762	11	O88521	O88521 rattus norv
25	77.5	13.2	1887	4	Q7Z3G4	Q7z3g4 homo sapien
26	77.5	13.2	1943	11	Q61307	Q61307 mus musculu
27	77.5	13.2	2622	11	O70511	O70511 rattus norv
28	77	13.1	316	16	Q9HXZ2	Q9hxz2 pseudomonas
29	77	13.1	1038	11	Q80ZZ7	Q80zz7 mus musculu
30	77	13.1	1050	11	Q8CCV0	Q8ccv0 mus musculu
31	77	13.1	1719	4	Q13768	Q13768 homo sapien
32	77	13.1	1856	4	Q99407	Q99407 homo sapien
33	76.5	13.0	364	12	Q68824	Q68824 hepatitis c
34	76.5	13.0	364	12	Q68805	Q68805 hepatitis c
35	76.5	13.0	388	16	Q97PS5	Q97ps5 streptococc
36	76	12.9	303	5	Q9NHG0	Q9nhg0 drosophila
37	76	12.9	536	16	Q9I2T7	Q9i2t7 pseudomonas
38	76	12.9	965	4	Q7Z344	Q7z344 homo sapien
39	76	12.9	1863	4	Q7Z3L5	Q7z3l5 homo sapien
40	75.5	12.9	319	6	Q9TV79	Q9tv79 oryctolagus
41	75.5	12.9	320	6	Q9XS29	Q9xs29 oryctolagus
42	75.5	12.9	356	10	Q8GRN3	Q8grn3 oryza sativ
43	75.5	12.9	364	12	O92543	O92543 hepatitis c
44	75.5	12.9	364	12	O92538	O92538 hepatitis c
45	75.5	12.9	811	4	Q9H0P5	Q9h0p5 homo sapien

ALIGNMENTS

RESULT 1

Q95ND3 ID Q95ND3 PRELIMINARY; PRT; 446 AA.

AC Q95ND3; 01-DEC-2001 (TremBLrel. 19, Created)

DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)

DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)

DE Tumor necrosis factor type I.

GN TNFR I.

OS Felis silvestris catus (Cat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.

OX NCBI\_TaxID=9685;

RN [1]

RP SEQUENCE FROM N.A.

RA Mizuno T., Goto Y., Baba K., Masuda K., Ohno K., Tsujimoto H.;

RT "Molecular cloning of feline tumor necrosis factor receptor type I (TNFR I) and expression of TNFR I and TNFR II in various disease in cats.";

RT Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.

RL EMBL; AB051103; BAB55455.1; --

DR GO; GO:0005489; F:electron transporter activity; IEA.

DR GO; GO:0004872; F:receptor activity; IEA.

DR GO; GO:0006118; P:electron transport; IEA.

DR GO; GO:0007165; P:signal transduction; IEA.

DR InterPro; IPR000345; CytC\_heme\_BS.

DR InterPro; IPR000488; Death.

DR InterPro; IPR006209; EGF like.

DR InterPro; IPR001368; TNFR\_c6.

DR Pfam; PF00531; death; 1.

DR Pfam; PF00020; TNFR\_c6; 4.

DR SMART; SM00005; DEATH; 1.

DR SMART; SM00208; TNFR; 4.

DR PROSITE; PS00190; CYTOCHROME\_C; 1.

DR PROSITE; PS50017; DEATH\_DOMAIN; 1.

DR PROSITE; PS01186; EGF\_2; 1.

DR PROSITE; PS00652; TNFR\_NGFR\_1; 3.

DR PROSITE; PS50050; TNFR\_NGFR\_2; 3.

SQ SEQUENCE 446 AA; 49563 MW; 217BD331DD8A74AA CRC64;













RT "The entire nucleotide sequence and classification of a hepatitis C  
RT virus isolate of a novel genotype from an Indonesian patient with  
RT chronic liver disease.";  
RL J. Gen. Virol. 75:629-635(1994).  
CC -!- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A  
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:  
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF  
CC PROTEIN C AND MRNA (BY SIMILARITY).  
DR EMBL; D14853; BAA03581.1; -.  
DR PIR; PQ0804; PQ0804.  
DR HSSP; P26663; IJXP.  
DR MEROPS; S29.001; -.  
DR MEROPS; U39.001; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019028; C:viral capsid; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0008026; F:ATP dependent helicase activity; IEA.  
DR GO; GO:0003723; F:RNA binding; IEA.  
DR GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.  
DR GO; GO:0008236; F:serine-type peptidase activity; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR GO; GO:0016740; F:transferase activity; IEA.  
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
DR GO; GO:0006350; P:transcription; IEA.  
DR GO; GO:0019079; P:viral genome replication; IEA.  
DR GO; GO:0019087; P:viral transformation; IEA.  
DR InterPro; IPR009003; Cys\_Ser\_trypsin.  
DR InterPro; IPR001410; DEAD.  
DR InterPro; IPR002522; HCV\_capsid.  
DR InterPro; IPR002519; HCV\_env.  
DR InterPro; IPR002531; HCV\_NS1.  
DR InterPro; IPR002518; HCV\_NS2.  
DR InterPro; IPR002517; HCV\_NS3.  
DR InterPro; IPR002516; HCV\_NS4.  
DR InterPro; IPR002515; HCV\_NS5.  
DR SEQUENCE 3011 AA; 327212 MW; 9C16C120F4E79268 CRC64;  
KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;  
KW Polyprotein; RNA-directed RNA polymerase; Transferase; Transmembrane.  
FT CHAIN 1 191  
FT CHAIN 192 383  
FT CHAIN 384 809  
FT CHAIN 810 1006  
FT CHAIN 1007 1657  
FT CHAIN 1658 1972  
FT CHAIN 1973 3011  
SQ SEQUENCE 3011 AA; 327212 MW; 9C16C120F4E79268 CRC64;  
Query Match 13.9%; Score 81.5; DB 12; Length 3011;  
Best Local Similarity 27.8%; Pred. No. 26;  
Matches 35; Conservative 11; Mismatches 39; Indels 41; Gaps 6;  
QY 3 HKPQSLDTPATLYAVVENVPLRWKEFKRL-GL-----SDHEIDRLQLNGRCL 53  
Db 2858 HLEKALDCE---IYGAVHSVQPLDLPEIIQRLHGLSAFSLHSYSPGEINRV----AACL 2909  
QY 54 REAQYSMLATWRRRTPRREATLELLGRVLRMDMLGLCLEDIEEALCG-----PAA 103

Db 2910 RKLGVPPPLRAWRHARSVRATLLSQGG-----RAAICGKYLENWA VKTKLK 2955  
QY 104 LPPAPS 109  
Db 2956 LTPLPS 2961  
RESULT 13  
Q68798  
ID Q68798 PRELIMINARY; PRT; 3022 AA.  
AC Q68798;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Genome polyprotein.  
OS Hepatitis C virus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
OC Hepacivirus.  
OX NCBI\_TaxID=11103;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=JK046;  
RX MEDLINE=96226020; PubMed=8627233;  
RA Tokita H., Okamoto H., Iizuka H., Kishimoto J., Tsuda F.,  
RA Lesmana L.A., Miyakawa Y., Mayumi M.;  
RT "Hepatitis C virus variants from Jakarta, Indonesia classifiable into  
RT novel genotypes in the second (2e and 2f), tenth (10a) and eleventh  
RT (11a) genetic groups.";  
RL J. Gen. Virol. 77:293-301(1996).  
CC -!- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A  
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:  
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF  
CC PROTEIN C AND MRNA (BY SIMILARITY).  
DR EMBL; D63822; BAA09891.1; -.  
DR HSSP; P27958; IHEI.  
DR MEROPS; S29.001; -.  
DR MEROPS; U39.001; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019028; C:viral capsid; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0008026; F:ATP dependent helicase activity; IEA.  
DR GO; GO:0003723; F:RNA binding; IEA.  
DR GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.  
DR GO; GO:0008236; F:serine-type peptidase activity; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR GO; GO:0016740; F:transferase activity; IEA.  
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
DR GO; GO:0006350; P:transcription; IEA.  
DR GO; GO:0019079; P:viral genome replication; IEA.  
DR GO; GO:0019087; P:viral transformation; IEA.  
DR InterPro; IPR009003; Cys\_Ser\_trypsin.  
DR InterPro; IPR001410; DEAD.  
DR InterPro; IPR002522; HCV\_capsid.  
DR InterPro; IPR002521; HCV\_core.  
DR InterPro; IPR002519; HCV\_env.  
DR InterPro; IPR002531; HCV\_NS1.  
DR InterPro; IPR002518; HCV\_NS2.  
DR InterPro; IPR000745; HCV\_NS4a.  
DR InterPro; IPR001490; HCV\_NS4b.  
DR InterPro; IPR002868; HCV\_NS5a.  
DR InterPro; IPR002166; HCV\_RdRP.  
DR InterPro; IPR004109; Peptidase\_C29.  
DR InterPro; IPR007095; RNA\_pol\_DS\_PS.  
DR InterPro; IPR007094; RNA\_pol\_PSVir.  
DR Pfam; PF01543; HCV\_capsid; 1.  
DR Pfam; PF01542; HCV\_core; 1.  
DR Pfam; PF01539; HCV\_env; 1.  
DR Pfam; PF01560; HCV\_NS1; 1.  
DR Pfam; PF01538; HCV\_NS2; 1.  
DR Pfam; PF02907; HCV\_NS3; 1.  
DR Pfam; PF01006; HCV\_NS4a; 1.  
DR Pfam; PF01001; HCV\_NS4b; 1.  
DR Pfam; PF01506; HCV\_NS5a; 1.  
DR Pfam; PF00998; Viral\_RdRP; 1.  
DR ProDom; PD186062; HCV\_NS1; 1.  
DR SMART; SM00487; DEXDc; 1.  
KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;  
KW Polyprotein; RNA-directed RNA polymerase; Transferase; Transmembrane.  
FT CHAIN 1 191  
FT CHAIN 192 383  
FT CHAIN 384 809  
FT CHAIN 810 1006  
FT CHAIN 1007 1657  
FT CHAIN 1658 1972  
FT CHAIN 1973 3011  
SQ SEQUENCE 3011 AA; 327212 MW; 9C16C120F4E79268 CRC64;  
Query Match 13.9%; Score 81.5; DB 12; Length 3011;  
Best Local Similarity 27.8%; Pred. No. 26;  
Matches 35; Conservative 11; Mismatches 39; Indels 41; Gaps 6;  
QY 3 HKPQSLDTPATLYAVVENVPLRWKEFKRL-GL-----SDHEIDRLQLNGRCL 53  
Db 2858 HLEKALDCE---IYGAVHSVQPLDLPEIIQRLHGLSAFSLHSYSPGEINRV----AACL 2909  
QY 54 REAQYSMLATWRRRTPRREATLELLGRVLRMDMLGLCLEDIEEALCG-----PAA 103









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OM protein - protein search, using sw model

Run on: June 1, 2004, 14:30:06 ; Search time 48.521 Seconds  
(without alignments)  
646.376 Million cell updates/sec

Title: US-09-854-906-8  
Perfect score: 582  
Sequence: 1 AHKPQSLDTDDPATLYAVVE.....DIEEALCGPAALPPAPSLLR 111

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A Geneseq\_29Jan04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	582	100.0	111	5	ABB81749 Tumour ne
2	582	100.0	158	5	ABG70127 Human pre
3	582	100.0	426	7	ABW00828 Human p55
4	582	100.0	453	4	AAB50895 Human TNF
5	582	100.0	455	2	ABG74755 Human TNF
6	582	100.0	455	2	AAR07451 Human Tum
7	582	100.0	455	2	ABG74751 Human TNF
8	582	100.0	455	2	AAR12550 Type I TN
9	582	100.0	455	2	AAR10986 30kD TNF
10	582	100.0	455	2	AAR11082 Human 55k
11	582	100.0	455	2	AAR20787 TNF-alpha
12	582	100.0	455	2	AAR42059 Lambda de
13	582	100.0	455	2	AAR51034 Mutant p5
14	582	100.0	455	2	AAR42197 p55 Tumou
15	582	100.0	455	2	AAR75084 p55 TNF-R
16	582	100.0	455	2	AAY30934 Human tum
17	582	100.0	455	3	AAB01336 TNF-R1 de
18	582	100.0	455	3	AAB26984 Human TNF
19	582	100.0	455	3	AAB36266 Human tum
20	582	100.0	455	3	AAB23446 Human tum
21	582	100.0	455	3	AAB37800 Human tum
22	582	100.0	455	4	AAB86817 Human TNF
23	582	100.0	455	4	AAB37677 Human 30
24	582	100.0	455	4	AAB36697 Human tum
25	582	100.0	455	5	AAU75064 Human tum

26	582	100.0	455	5	AAO22286	TNFR1 exp
27	582	100.0	455	5	ABB81649	Human tum
28	582	100.0	455	5	ABP54799	Human COP
29	582	100.0	455	6	ABP70914	Human CON
30	582	100.0	455	6	ABR58539	Human tum
31	582	100.0	455	6	ADA20581	Precursor
32	582	100.0	455	7	ADE57929	Human Pro
33	582	100.0	909	2	AAW64485	Human Fas
34	579	99.5	112	5	ABB81751	Tumour ne
35	557	95.7	455	2	AAR24000	TNF-alpha
36	521	89.5	443	2	AAR51033	Mutant p5
37	469	80.6	433	2	AAR51032	Mutant TNF
38	446	76.6	86	4	AAV97655	Human TNF
39	446	76.6	108	2	AAW73570	Cytoplasm
40	424	72.9	471	5	ABB98169	Bovine tu
41	424	72.9	471	5	AAE25816	Bovine tu
42	407	69.9	78	5	ABG31493	Human Apo
43	407	69.9	78	6	ADA49709	Death dom
44	397.5	68.3	84	2	AAW62179	Tumour ne
45	386	66.3	461	2	ABG74754	Rat TNF-R

ALIGNMENTS

RESULT 1  
ABB81749  
ID ABB81749 standard; protein; 111 AA.  
XX  
AC ABB81749;  
XX  
DT 10-SEP-2002 (first entry)  
XX  
DE Tumour necrosis factor receptor 1 death domain (shorter sequence).  
XX  
KW Tumour necrosis factor receptor 1; receptor; TNFR-1; death domain;  
KW receptor signalling; TNFR-1 DD; protein co-ordinate data.  
XX  
OS Unidentified.  
XX  
FH Key Location/Qualifiers  
FT Region 15..21 /label= Alpha\_helix\_1  
FT Region 28..34 /label= Alpha\_helix\_2  
FT Region 38..42 /label= Alpha\_helix\_3  
FT Region 52..65 /label= Alpha\_helix\_4  
FT Region 72..85 /label= Alpha\_helix\_5  
FT Region 89..98 /label= Alpha\_helix\_6  
XX  
US2002045578-A1.  
XX  
PD 18-APR-2002.  
XX  
PF 14-MAY-2001; 2001US-00854906.  
XX  
PR 22-MAY-2000; 2000US-0206215P.  
XX  
PA (SUKI/) SUKITS S F.  
PA (XUGG/) XU G.  
PA (LINL/) LIN L.  
PA (TELL/) TELLIEZ J.  
PA (HSUS/) HSU S.  
XX  
PI Sukits SF, Xu G, Lin L, Telliez J, Hsu S;  
XX  
DR WPI; 2002-443412/47.  
XX  
PT Solution comprising tumor necrosis factor receptor 1 death domain, useful

for identifying potential inhibitor of tumor necrosis factor receptor 1 death domain.

Claim 1; Fig 4; 49pp; English.

The sequence represents the tumour necrosis factor receptor 1 death domain (TNFR-1 DD), which is the intracellular functional domain responsible for the receptor signalling activities. The invention relates to a novel solution comprising a tumour necrosis factor receptor 1 death domain. The solution is useful for identifying a potential inhibitor of TNFR-1 DD, for the design and selection of potent and selective inhibitors of TNF signalling pathways, and for generating a three-dimensional structure for an unknown molecule or molecular complex

Sequence 111 AA;

compound that inhibits or activates the protein-protein interactions; (3) a modulating compound obtained from the method of (2); (4) a SID (selected interacting domain) polypeptide or its fragment or variant comprising the human polypeptides appearing as ABG70042-ABG70242; (5) a SID polynucleotide or its fragment or variant comprising encoding the above polypeptides a vector comprising (5); (6) a recombinant host cell containing the vector; and (10) a protein chip comprising Shigella flexneri polypeptide and a mammalian polypeptide defined in the specification. A pharmaceutical composition comprising the compound, polypeptide or polynucleotide is useful for treating or preventing shigellosis (bacillary dysentery) in a human or mammal. The present sequence represents a human prey protein isolated by the yeast two-hybrid assay, forming a complex of the invention with a shigella protein

Sequence 158 AA;

CC polypeptide capable of binding to an intracellular domain of a p55 tumour  
CC necrotic factor (TNF) receptor. The DNA molecule is useful for preparing  
CC a composition for treating tumour, rheumatoid arthritis or inflammatory  
CC diseases. The invention is useful in gene therapy. The present sequence  
CC is the human p55IC-R protein  
XX  
SQ Sequence 426 AA;

Query Match 100.0%; Score 582; DB 7; Length 426;  
Best Local Similarity 100.0%; Pred. No. 8.3e-61;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AHKQSLDITDDPATLYAVVENVPLRWKEFVRLGLSDHEIDRLQLNGRCLREAQYSML 60  
Db 316 AHKQSLDITDDPATLYAVVENVPLRWKEFVRLGLSDHEIDRLQLNGRCLREAQYSML 375  
QY 61 ATWRRTPRREATLELLGRVLRDMDLLGCLDIEEALCGPAALPPAPSLR 111  
Db 376 ATWRRTPRREATLELLGRVLRDMDLLGCLDIEEALCGPAALPPAPSLR 426

RESULT 4  
AAB50895  
ID AAB50895 standard; protein; 453 AA.  
XX  
AC AAB50895;  
XX  
DT 19-MAR-2001 (first entry)  
XX  
DE Human TNFR 1.

XX Human; TR10 receptor; cytostatic; immunosuppressive; neuroprotective;  
KW antiinflammatory; anti-HIV; antiparkinsonian; nootropic; cardiant;  
KW vasotropic; antiallergic; antidiabetic; vulnery; ophthalmological;  
KW antiviral; antibacterial; antifungal; antiparasitic; gene therapy; TNFR;  
KW tumour necrosis factor receptor; cancer; leukaemia; autoimmune disorder;  
KW apoptosis; cardiovascular disorder; inflammatory disease; wound;  
KW infection; neurological disease; protein coordinate data.  
XX  
OS Homo sapiens.  
XX  
PN WO200073321-A1.  
XX  
PD 07-DEC-2000.  
XX  
PF 26-MAY-2000; 2000WO-US014554.  
XX  
PR 28-MAY-1999; 99US-0136786P.  
PR 07-JUL-1999; 99US-0142563P.  
PR 15-JUL-1999; 99US-0144023P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Rosen CA, Ni J;  
XX  
DR WPI; 2001-025250/03.

XX Nucleic acid encoding a tumor necrosis factor receptor 10, useful in the  
PT diagnosis, treatment or prevention of cancer, autoimmune disorders, and  
PT diseases and disorders associated with apoptosis.  
XX  
PS Disclosure; Fig 2; 212pp; English.

XX The present sequence is given in a specification relating to an isolated  
CC nucleic acid encoding a human tumour necrosis factor receptor TR10. The  
CC TR10 polynucleotide, polypeptide, antibodies, agonists and antagonists  
CC are useful in the diagnosis, treatment or prevention of cancer, such as  
CC breast and ovarian cancer and leukaemia; autoimmune disorders such as  
CC multiple sclerosis, Crohn's disease and graft versus host disease;  
CC diseases associated with increased apoptosis such as AIDS, Alzheimer's  
CC disease and Parkinson's disease; cardiovascular disorders such as limb  
CC ischaemia and congenital heart defects; inflammatory diseases e.g.  
CC allergy; wound healing; disorders associated with neovascularisation,

CC e.g. diabetic retinopathy; infectious diseases such as viral, bacterial,  
CC fungal and parasitic infections; and neurological diseases such as  
CC amyotrophic lateral sclerosis  
XX  
SQ Sequence 453 AA;

Query Match 100.0%; Score 582; DB 4; Length 453;  
Best Local Similarity 100.0%; Pred. No. 9e-61;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AHKQSLDITDDPATLYAVVENVPLRWKEFVRLGLSDHEIDRLQLNGRCLREAQYSML 60  
Db 343 AHKQSLDITDDPATLYAVVENVPLRWKEFVRLGLSDHEIDRLQLNGRCLREAQYSML 402  
QY 61 ATWRRTPRREATLELLGRVLRDMDLLGCLDIEEALCGPAALPPAPSLR 111  
Db 403 ATWRRTPRREATLELLGRVLRDMDLLGCLDIEEALCGPAALPPAPSLR 453

RESULT 5  
ABG74755  
ID ABG74755 standard; protein; 455 AA.  
XX  
AC ABG74755;  
XX  
DT 14-MAY-2003 (first entry)  
XX  
DE Human TNF-R protein huTNF-R.

XX TNF; human; tumour necrosis factor; tumour necrosis factor receptor;  
KW TNF-R; tumour necrosis factor binding protein; TNF-BP; tumour.  
XX Homo sapiens.  
PN EP393438-A.  
XX  
PD 24-OCT-1990.  
XX  
PF 06-APR-1990; 90EP-00106624.  
XX  
PR 21-APR-1989; 89DE-03913101.  
PR 21-JUN-1989; 89DE-03920282.  
XX  
PA (BOEH ) BOEHRINGER INGELHEIM INT GMBH.  
PA (SYND ) SYNERGEN INC.

XX Hauptmann R, Himmler A, Maurerfogy I, Stratowa C;  
DR WPI; 1990-321987/43.  
DR N-PSDB; ABQ77487.

XX DNA encoding TNF binding protein and TNF- receptor - used in tumour  
PT treatment and to understand mechanisms to TNF action.  
XX  
PS Example 9; Fig 9; 51pp; German.

XX This invention describes novel polynucleotide sequences encoding tumour  
CC necrosis factor (TNF) receptor (TNF-R) or TNF binding protein (TNF-BP).  
CC The products of the invention are useful in pharmaceutical compositions  
CC for prophylaxis or treatment of human tumours and to understand the  
CC mechanisms of TNF action. This sequence represents the huma TNF-R, huTNF-  
CC R described in the disclosure of the invention  
XX  
SQ Sequence 455 AA;

Query Match 100.0%; Score 582; DB 2; Length 455;  
Best Local Similarity 100.0%; Pred. No. 9e-61;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AHKQSLDITDDPATLYAVVENVPLRWKEFVRLGLSDHEIDRLQLNGRCLREAQYSML 60  
Db 345 AHKQSLDITDDPATLYAVVENVPLRWKEFVRLGLSDHEIDRLQLNGRCLREAQYSML 404



QY	61	ATWRRRTPRREATLELLGRVLRDMDLLGCLIEDIEEALCGPAALPPAPSLLR	111
Db	405	ATWRRRTPRREATLELLGRVLRDMDLLGCLIEDIEEALCGPAALPPAPSLLR	455
RESULT 6			
AAR07451			
ID	AAR07451	standard; protein; 455 AA.	
XX			
AC	AAR07451;		
XX			
DT	25-MAR-2003	(revised)	
DT	29-JAN-1991	(first entry)	
XX			
DE	Human Tumour Necrosis Factor-Receptor from lambdaTNF-R2 cDNA insert.		
XX			
KW	Tumour necrosis factor binding protein; TNF-BP; TNF-receptor;		
KW	infectious disease; parasitic disease; cachexia; autoimmune disease;		
KW	shock; lambdaTNF-R2; raTNF-R8.		
XX			
OS	Homo sapiens.		
XX			
PN	EP393438-A.		
XX			
PD	24-OCT-1990.		
XX			
PF	06-APR-1990;	90EP-00106624.	
XX			
PR	21-APR-1989;	89DE-03913101.	
PR	21-JUN-1989;	89DE-03920282.	
XX			
PA	(BOEH ) BOEHRINGER INGELHEIM INT GMBH.		
PA	(SYND ) SYNERGEN INC.		
XX			
PI	Hauptmann R, Himmler A, Maurerfogy I, Stratowa C;		
XX			
DR	WPI; 1990-321987/43.		
XX			
DR	N-PSDB; AAQ06285.		
XX			
PT	DNA encoding TNF binding protein and TNF- receptor - used in tumour		
PT	treatment and to understand mechanisms to TNF action.		
XX			
PS	Disclosure; Fig 91(1-2); 51pp; German.		
XX			
CC	raTNF-R8 (AAQ06284) was used to screen the HS913T cDNA library. LambdaTNF		
CC	-R2 encodes the complete human TNF-R2 and was used to construct a plasmid		
CC	(pADTNF-R) expressing the product the same way as pADTNF-BP (see		
CC	AAQ06282). The expressed proteins are useful prophylactically and		
CC	therapeutically to control disorders which involve the damaging effects		
CC	of TNF-alpha or -beta (e.g. infectious or parasitic diseases, shock,		
CC	cachexia, autoimmune diseases, adult respiratory distress syndrome etc.,		
CC	or side effects of treatment with TNG-alpha). They can also be used as		
CC	diagnostic reagents for assaying TNF and in study of TNF-receptor		
CC	interactions. See also AAQ06282-Q06285. (Updated on 25-MAR-2003 to		
CC	correct PA field.) (Updated on 25-MAR-2003 to correct PI field.)		
XX			
SQ	Sequence 455 AA;		
Query Match 100.0%; Score 582; DB 2; Length 455;			
Best Local Similarity 100.0%; Pred. No. 9e-61;			
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	AHKPQSLDTPATLYAVVENVPPLRWKEFVRRRLGLSDHEIDRLQLONGRCLREAQYSML	60
Db	345	AHKPQSLDTPATLYAVVENVPPLRWKEFVRRRLGLSDHEIDRLQLONGRCLREAQYSML	404
QY	61	ATWRRRTPRREATLELLGRVLRDMDLLGCLIEDIEEALCGPAALPPAPSLLR	111
Db	405	ATWRRRTPRREATLELLGRVLRDMDLLGCLIEDIEEALCGPAALPPAPSLLR	455
RESULT 8			
AAR12550			
ID	AAR12550	standard; protein; 455 AA.	
XX			
AC	AAR12550;		
XX			
DT	25-MAR-2003	(revised)	
DT	12-SEP-1991	(first entry)	
XX			
DE	Type I TNF receptor.		
XX			
KW	Tumour Necrosis Factor; TNF; binding protein; TBP-I.		
XX			
OS	Homo sapiens.		
XX			
FH	Key	Location/Qualifiers	
FT	Peptide	1. .21	



DT 09-JAN-2003 (revised)  
DT 24-MAY-1991 (first entry)  
XX  
DE Human 55kD TNF-binding protein.  
XX  
KW Tumour Necrosis Factor; binding proteins; septic shock;  
KW autoimmune glomerulonephritis; lymphokine; cytokine.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1. .28  
FT /label= signal peptide  
FT Modified-site 54  
FT /label= putative N-glycosylation site  
FT Modified-site 145  
FT /label= putative N-glycosylation site  
FT Modified-site 151  
FT /label= putative N-glycosylation site  
FT Region 212. .230  
FT /label= transmembrane region  
FT Modified-site 270  
FT /label= putative N-glycosylation site  
XX  
PN EP417563-A.  
XX  
PD 20-MAR-1991.  
XX  
PF 31-AUG-1990; 90EP-00116707.  
XX  
PR 12-SEP-1989; 89CH-00003319.  
PR 08-MAR-1990; 90CH-00000746.  
PR 20-APR-1990; 90CH-00001347.  
XX  
PA (HOFF ) HOFFMANN-LA ROCHE AG.  
XX  
PI Brockhaus M, Dembic Z, Gentz R, Lesslauer W, Lotscher H;  
PI Schlaeger EJ;  
XX  
DR WPI; 1991-081851/12.  
DR N-PSDB; AAQ10955.  
XX  
PT Insoluble tumour necrosis factor binding proteins - and DNA encoding  
PT them, useful in pharmaceutical prods. and for antibody prodn.  
XX  
PS Claim 1; Fig 1; 26pp; German.  
XX  
CC Partial amino acid sequences were determined for the 55 and 75kD TNF-BPs  
CC (see AAR11072-R11081) and oligonucleotide primers were synthesised based  
CC on these partial sequences. The primers were used to produce a cDNA  
CC fragment for use as a probe to screen a human placental cDNA bank  
CC constructed in lambda gt11. Positive clones were identified and sequenced.  
CC DNA constructs comprising the TNF-BP coding sequence may also contain a  
CC fragment encoding a human Ig domain. Recombinant constructs are used to  
CC transform cells to confer improved TNF-binding properties. See also  
CC AAQ10956. (Updated on 09-JAN-2003 to add missing OS field.)  
XX  
SQ Sequence 455 AA;

Query Match 100.0%; Score 582; DB 2; Length 455;  
Best Local Similarity 100.0%; Pred. No. 9e-61;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AHKPSLDTDDPATLYAVVENVPPLRWKEFVRRRLGSLDHEIDRLQLNGRCLREAQYSML 60  
Db |||||  
345 AHKPSLDTDDPATLYAVVENVPPLRWKEFVRRRLGSLDHEIDRLQLNGRCLREAQYSML 404  
QY 61 ATWRRRTPRREATLELLGRVLRDMDLLGCLDIEEALCGPAALPPAPSLLR 111  
Db |||||  
405 ATWRRRTPRREATLELLGRVLRDMDLLGCLDIEEALCGPAALPPAPSLLR 455

RESULT 11  
AAR42059

AAR20787  
ID AAR20787 standard; protein; 455 AA.  
XX  
AC AAR20787;  
XX  
DT 11-MAY-1992 (first entry)  
XX  
DE TNF-alpha binding protein.  
XX  
KW Tumour necrosis factor alpha; autoimmune diseases; cachectin;  
KW extracellular domain.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1. .40  
FT /note= "signal peptide"  
FT Domain 30. .199  
FT /note= "extracellular domain"  
FT Peptide 41. .455  
FT /note= "mature peptide"  
FT Modified-site 145. .147  
FT /note= "potential N-glycosylation site"  
FT Modified-site 151. .153  
FT /note= "potential N-glycosylation site"  
FT Domain 212. .234  
FT /note= "transmembrane domain"  
XX  
PN GB2246569-A.  
XX  
PD 05-FEB-1992.  
XX  
PF 15-JUN-1990; 90GB-00013410.  
XX  
PR 15-JUN-1990; 90GB-00013410.  
XX  
PA (CHAR-) CHARING CROSS SUNLE.  
XX  
PI Feldman M, Gray P, Turner M, Brennan F;  
XX  
DR WPI; 1992-043613/06.  
DR N-PSDB; AAQ20973.  
XX  
PT New tumour necrosis factor alpha binding protein and polypeptide - useful  
PT in treating cachexia, sepsis and auto immune diseases e.g. rheumatoid  
PT arthritis.  
XX  
PS Disclosure; Fig 1; 25pp; English.  
XX  
CC The amino acid sequence is that of tumour necrosis factor alpha binding  
CC protein which contains the extracellular domain of human TNF alpha  
CC receptor. It is soluble and can be used in the regulation of TNF-mediated  
CC responses by binding and sequestering the cytokine. It can therefore be  
CC used therapeutically to treat disorders such as cachexia, sepsis and  
CC autoimmune diseases, specifically rheumatoid arthritis  
XX  
SQ Sequence 455 AA;

Query Match 100.0%; Score 582; DB 2; Length 455;  
Best Local Similarity 100.0%; Pred. No. 9e-61;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AHKPSLDTDDPATLYAVVENVPPLRWKEFVRRRLGSLDHEIDRLQLNGRCLREAQYSML 60  
Db |||||  
345 AHKPSLDTDDPATLYAVVENVPPLRWKEFVRRRLGSLDHEIDRLQLNGRCLREAQYSML 404  
QY 61 ATWRRRTPRREATLELLGRVLRDMDLLGCLDIEEALCGPAALPPAPSLLR 111  
Db |||||  
405 ATWRRRTPRREATLELLGRVLRDMDLLGCLDIEEALCGPAALPPAPSLLR 455

RESULT 12  
AAR42059

ID AAR42059 standard; protein; 455 AA.  
XX AAR42059;  
AC  
XX 27-AUG-2003 (revised)  
DT 25-MAR-2003 (revised)  
XX 29-APR-1994 (first entry)  
DE  
XX Lambda derived TNF-R.  
DE  
XX Human; tumour necrosis factor receptor; TNF-R; interleukin-1 receptor;  
KW IL-1R; fusion protein; linker; TNF; IL-1; cachexia; cerebral malaria;  
KW rheumatoid arthritis; diabetes; multiple sclerosis; septic shock;  
KW pulmonary fibrosis; silicosis; allograft; xenograft; rejection;  
KW graft verses host disease; sepsis; inflammation; allergy;  
KW autoimmune dysfunction.  
XX  
XX Homo sapiens.  
OS Bacteriophage lambda.  
OS  
XX  
XX Key Location/Qualifiers  
FH Peptide 1..40  
FT /note= "Signal peptide"  
FT 41..455  
FT /note= "Mature hTNF-R"  
FT  
XX WO9319777-A1.  
PN  
XX 14-OCT-1993.  
PD  
XX 26-MAR-1993; 93WO-US002938.  
PF  
XX 30-MAR-1992; 92US-00860710.  
PR  
XX (IMMV ) IMMUNEX CORP.  
PA  
XX Smith CA;  
PI  
XX WPI; 1993-336592/42.  
DR N-PSDB; AAQ49932.  
XX  
XX New fusion protein tumour necrosis factor and human interleukin-1  
PT receptor - useful in therapy, diagnosis and assays of e.g. rheumatoid  
PT arthritis, diabetes, cerebral malaria, sepsis, etc.  
XX  
PS Disclosure; Page 57-59; 85pp; English.  
XX  
CC The sequences given in AAR42058-59 represent human tumour necrosis  
CC factor receptor (TNF-R) and the sequences in AAR42060-61 represent human  
CC interleukin-1 receptor (IL-1R). These sequences were used in the  
CC production of a fusion protein which conformed to one of the formulae:  
CC TNF-R-linker-TNF-R-linker-IL-1R IL-1R-linker-TNF-R-linker-TNF-R or TNF-R-  
CC linker-TNF-R The linker may comprise 5-100 amino acids selected from Gly,  
CC Asp, Ser, Thr and Ala. These linkers separate the individual moieties by  
CC such a distance that each component of the fusion protien is capable of  
CC folding into the secondary or tertiary structure required for its  
CC biological activity. These fusion proteins may be used in therapy,  
CC diagnosis and assays for conditions mediated by TNF or IL-1, particularly  
CC in conditions in which both TNF and IL-1 play a causative role. They may  
CC be used to treat cachexia, rheumatoid arthritis, diabetes, multiple  
CC sclerosis, pulmonary fibrosis and silicosis, cerebral malaria, allograft  
CC and xenograft rejection in graft verses host disease, sepsis, septic  
CC shock, inflammation, allergies and autoimmune dysfunctions. (Updated on  
CC 25-MAR-2003 to correct PN field.) (Updated on 27-AUG-2003 to correct OS  
CC field.)  
XX  
SQ Sequence 455 AA;  
  
Query Match 100.0%; Score 582; DB 2; Length 455;  
Best Local Similarity 100.0%; Pred. No. 9e-61;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 345 AHKPSQSLDTPATLYAVVENVPLRWKEFVRRGLSDHEIDRLQLNGRCLREAQYSML 404  
QY 61 ATWRRRTPRREATIELLGRVLRDMDLLGCLLEIEEALCGPAALPPAPSLR 111  
Db 405 ATWRRRTPRREATIELLGRVLRDMDLLGCLLEIEEALCGPAALPPAPSLR 455  
  
RESULT 13  
AAR51034  
ID AAR51034 standard; protein; 455 AA.  
XX  
AC AAR51034;  
XX  
DT 25-MAR-2003 (revised)  
DT 13-MAY-1994 (first entry)  
XX  
DE Mutant p55 tumour necrosis factor receptor.  
XX  
KW TNF; tumour necrosis factor; receptor; disease; autoimmunity;  
KW rheumatoid arthritis; graft rejection; graft vs. host; septic shock;  
KW effector protein.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Region 1..21  
FT /label= Leader peptide.  
FT Domain 183..205  
FT /label= Transmembrane domain.  
XX  
PN EP568925-A2.  
XX  
PD 10-NOV-1993.  
XX  
PF 29-APR-1993; 93EP-00106981.  
XX  
PR 03-MAY-1992; 92IL-00101769.  
XX  
PA (YEDA ) YEDA RES & DEV CO LTD.  
XX  
PI Wallach D; Brakebusch C;  
XX  
DR WPI; 1993-353057/45.  
DR N-PSDB; AAQ50870.  
XX  
PT Modulating activity of tumour necrosis factor receptor - using  
PT peptide(s), antibodies, etc. which interact with critical regions of  
PT receptor or effector protein, for controlling auto-immune disease, septic  
PT shock, etc.  
XX  
PS Claim 5; Fig 1; 17pp; English.  
XX  
CC Modification of the tumour necrosis factor receptor by mutation or  
CC deletion modulates signal transduction and/or cleavage effected by the  
CC receptor. This modulation of activity can also be achieved using effector  
CC proteins which interact with the TNF receptor. Molecules which interact  
CC with the TNF receptor or the effector proteins can be used to treat or  
CC prevent diseases associated with TNF activity e.g. autoimmune disease;  
CC rheumatoid arthritis; graft rejection; graft vs. host disease or septic  
CC shock. They can also be used to treat overdoses of exogenous TNF.  
CC Specific deletions include amino acid residues 405-426 from which it was  
CC discovered that amino acids 405-414, or part of them, are essential for  
CC the signalling of the human p55 TNF-R for the cytotoxic effect of TNF  
CC whereas amino acids 415-426 are not essential. Also residues 170-174, 174  
CC -179 or both i.e 170-179 were deleted. This region of amino acids, or  
CC part of, when deleted, abolished shedding of the soluble extracellular  
CC forms of the protein. This sequence corresponds to the wild type protein  
CC disclosed in AAR42197 except that alanine at position 197 has been  
CC substituted in place of serine. The substitution inhibits cleavage of the  
CC soluble form of the protein. (Updated on 25-MAR-2003 to correct PN  
XX field.)



SQ Sequence 455 AA;  
Query Match 100.0%; Score 582; DB 2; Length 455;  
Best Local Similarity 100.0%; Pred. No. 9e-61;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AHKPSLDTDDPATLYAVVENPPLRWKEFVRRRLGSLDHEIDRLQLNGRCLREAYSM 60  
Db 345 AHKPSLDTDDPATLYAVVENPPLRWKEFVRRRLGSLDHEIDRLQLNGRCLREAYSM 404  
QY 61 ATWRRRTPRREATLELLGRVLRDMDLLGCLDIEEALCGPAALPPAPSLR 111  
Db 405 ATWRRRTPRREATLELLGRVLRDMDLLGCLDIEEALCGPAALPPAPSLR 455  
RESULT 14  
AAR42197  
ID AAR42197 standard; protein; 455 AA.  
AC AAR42197;  
XX 25-MAR-2003 (revised)  
DT 13-MAY-1994 (first entry)  
XX p55 Tumour necrosis factor receptor.  
DE TNF; tumour necrosis factor; receptor; disease; autoimmunity;  
XX rheumatoid arthritis; graft rejection; graft vs. host; septic shock;  
KW effector protein.  
KW Homo sapiens.  
OS Key Location/Qualifiers  
FH Region 1..21  
FT /label= Leader peptide.  
FT Domain 183..205  
FT /label= Transmembrane domain.  
XX EP568925-A2.  
PN 10-NOV-1993.  
XX 29-APR-1993; 93EP-00106981.  
PF 03-MAY-1992; 92IL-00101769.  
XX (YEDA ) YEDA RES & DEV CO LTD.  
PA Wallach D, Brakebusch C;  
XX Modulating activity of tumour necrosis factor receptor - using  
PT peptide(s), antibodies, etc. which interact with critical regions of  
PT receptor or effector protein, for controlling auto-immune disease, septic  
PT shock, etc.  
XX Claim 2; Fig 1; 17pp; English.  
XX Modification of the tumour necrosis factor receptor by mutation or  
CC deletion modulates signal transduction and/or cleavage effected by the  
CC receptor. This modulation of activity can also be achieved using effector  
CC proteins which interact with the TNF receptor. Molecules which interact  
CC with the TNF receptor or the effector proteins can be used to treat or  
CC prevent diseases associated with TNF activity e.g. autoimmune disease;  
CC rheumatoid arthritis; graft rejection; graft vs. host disease or septic  
CC shock. They can also be used to treat overdoses of exogenous TNF.  
CC Specific deletions include amino acid residues 405-426 from which it was  
CC discovered that amino acids 405-414, or part of them, are essential for  
CC the signalling of the human p55 TNF-R for the cytotoxic effect of TNF  
CC whereas amino acids 415-426 are not essential. Also residues 170-174, 174  
CC -179 or both i.e 170-179 were deleted. This region of amino acids, or

CC part of, when deleted, abolished shedding of the soluble extracellular  
CC forms of the protein. (Updated on 25-MAR-2003 to correct PN field.)  
XX Sequence 455 AA;  
SQ Query Match 100.0%; Score 582; DB 2; Length 455;  
Best Local Similarity 100.0%; Pred. No. 9e-61;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AHKPSLDTDDPATLYAVVENPPLRWKEFVRRRLGSLDHEIDRLQLNGRCLREAYSM 60  
Db 345 AHKPSLDTDDPATLYAVVENPPLRWKEFVRRRLGSLDHEIDRLQLNGRCLREAYSM 404  
QY 61 ATWRRRTPRREATLELLGRVLRDMDLLGCLDIEEALCGPAALPPAPSLR 111  
Db 405 ATWRRRTPRREATLELLGRVLRDMDLLGCLDIEEALCGPAALPPAPSLR 455  
RESULT 15  
AAR75084  
ID AAR75084 standard; protein; 455 AA.  
XX AAR75084;  
AC AAR75084;  
XX 19-JAN-1996 (first entry)  
DT p55 TNF-R.  
DE p55; tumour necrosis factor receptor; TNF-R; human; murine; chimera;  
XX epidermal growth factor receptor; EGF-R; protease; inhibitor;  
KW phorbol myristate acetate; PMA.  
KW Homo sapiens.  
OS Key Location/Qualifiers  
FH Peptide 41..53  
FT /note= "N terminus of soluble p55 TNF-R"  
FT Modified-site 54..56  
FT /note= "glycosylation site"  
FT Modified-site 145..147  
FT /note= "glycosylation site"  
FT Modified-site 161..163  
FT /note= "glycosylation site"  
FT Peptide 193..210  
FT /note= "peptide used in creation of chimeras"  
FT Region 198..210  
FT /note= "spacer region"  
FT Misc-difference 201  
FT /note= "major C terminus for soluble p55 TNF-R"  
FT Misc-difference 202  
FT /note= "essential for shedding reaction"  
FT Misc-difference 203  
FT /note= "minor C terminus for soluble p55 TNF-R"  
FT Region 212..234  
FT /note= "transmembrane region"  
XX AU9475742-A.  
PN 04-MAY-1995.  
PD 11-OCT-1994; 94AU-00075742.  
XX 12-OCT-1993; 93IL-00107268.  
XX (YEDA ) YEDA RES & DEV CO LTD.  
PA Wallach D, Brakebusch C, Varfolomeev E, Batkin M;  
PI WPI; 1995-194342/26.  
XX N-PSDB; AAQ90513.  
DR New protease capable of cleaving soluble tumour necrosis factor (TNF)  
DR receptor - from cell-bound TNF- receptor, useful for antagonising

PT deleterious effects of TNF.

PS Disclosure; Fig 1; 40pp; English.

This sequence represents human p55 tumour necrosis factor (TNF-R). Expression of this receptor is regulated by shedding of the extracellular receptor fragment. The p55 TNF-R can be shed in response to different inducing agents, e.g. phorbol myristate acetate (PMA), depending on cell type. The only region of the receptor whose structure affects the shedding response is the spacer region (see AAR75012) in the extracellular domain. This region is located close to a site of cleavage of the molecule, and links the Cys rich module to the transmembrane domain. The spacer region of the encoded protein was used to create the chimeras between human p55 TNF-R and murine epidermal growth factor receptor (EGF-R) that are represented by AAR75007-11. This spacer region was subjected to deletion mutations (AAR75013-25) and substitutions (AAR75026-47). Of the spacer region, the most important residues are Asn 172, Val 173, Lys 174 and Gly 175, with Val 173 being the most important of these. The shedding of the receptor is independent of the side chain identity of these residues, with the exception of a limited dependence on the identity of Val 173. Mutations which alter the conformation of the protein adversely effect the shedding process. The mutations shown in AAR75013-47 were introduced in order to create an inhibitor of a protease that is capable of cleaving the soluble TNF-R from the cell bound TNF-R. Fragments of these inhibitors can be seen in AAR75017-9, AAR75025, AAR75033-5 and AAR75042-3. These protease inhibitors can be used for enhancing TNF function

SQ Sequence 455 AA;

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Query Match          100.0%; Score 582; DB 2; Length 455;
Best Local Similarity 100.0%; Pred. No. 9e-61;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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[illegible]

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Search completed: June 1, 2004, 14:43:52
Job time : 48.521 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 1, 2004, 14:41:22 ; Search time 13.9581 Seconds  
(without alignments)  
410.549 Million cell updates/sec

Title: US-09-854-906-8  
Perfect score: 582  
Sequence: 1 AHKQSLDITDPAIYAVWE.....DIEEALCGPAALPPAPSLLR 111

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	582	100.0	426	4	US-08-747-562-37 Sequence 37, Appl
2	582	100.0	453	3	US-09-086-483A-5 Sequence 5, Appli
3	582	100.0	453	4	US-09-580-212-5 Sequence 5, Appli
4	582	100.0	453	4	US-09-769-402-5 Sequence 5, Appli
5	582	100.0	455	1	US-08-321-668-2 Sequence 2, Appli
6	582	100.0	455	1	US-08-837-941-2 Sequence 2, Appli
7	582	100.0	455	2	US-08-126-016-2 Sequence 2, Appli
8	582	100.0	455	3	US-08-815-469-5 Sequence 5, Appli
9	582	100.0	455	3	US-09-006-353A-3 Sequence 3, Appli
10	582	100.0	455	4	US-09-527-236A-5 Sequence 5, Appli
11	582	100.0	455	4	US-08-054-970-2 Sequence 2, Appli
12	582	100.0	455	4	US-09-565-918-4 Sequence 4, Appli
13	582	100.0	455	4	US-09-573-986-3 Sequence 3, Appli
14	582	100.0	455	4	US-09-027-287-3 Sequence 3, Appli
15	582	100.0	455	4	US-09-252-656B-3 Sequence 3, Appli
16	582	100.0	455	4	US-08-406-824A-4 Sequence 4, Appli
17	582	100.0	455	4	US-09-523-323-3 Sequence 3, Appli
18	582	100.0	455	4	US-09-756-854-5 Sequence 5, Appli
19	582	100.0	909	4	US-09-013-895A-4 Sequence 4, Appli
20	582	100.0	909	4	US-09-448-868-4 Sequence 4, Appli
21	577	99.1	455	1	US-08-050-319B-25 Sequence 25, Appl
22	577	99.1	455	2	US-08-465-982-25 Sequence 25, Appl
23	446	76.6	86	3	US-09-042-785A-25 Sequence 25, Appl
24	446	76.6	108	2	US-08-580-988A-20 Sequence 20, Appl
25	424	72.9	471	4	US-09-513-007-2 Sequence 2, Appli
26	407	69.9	78	4	US-08-828-683A-23 Sequence 23, Appl
27	397.5	68.3	84	4	US-09-069-827A-120 Sequence 120, App

28	366	62.9	70	4	US-09-159-277A-6 Sequence 6, Appli
29	343.5	59.0	68	4	US-09-527-236A-23 Sequence 23, Appl
30	343.5	59.0	68	4	US-09-756-854-23 Sequence 23, Appl
31	329	56.5	64	4	US-08-894-626-3 Sequence 3, Appli
32	235	40.4	45	2	US-08-219-237B-11 Sequence 11, Appl
33	213	36.6	41	1	US-08-444-005-29 Sequence 29, Appl
34	192	33.0	41	1	US-08-444-005-23 Sequence 23, Appl
35	176	30.2	41	1	US-08-444-005-28 Sequence 28, Appl
36	168	28.9	833	4	US-09-013-895A-5 Sequence 5, Appli
37	168	28.9	833	4	US-09-448-868-5 Sequence 5, Appli
38	167.5	28.8	417	3	US-08-815-469-4 Sequence 4, Appli
39	167.5	28.8	417	3	US-09-153-927-2 Sequence 2, Appli
40	167.5	28.8	417	4	US-09-565-918-5 Sequence 5, Appli
41	167.5	28.8	417	4	US-08-928-069-10 Sequence 10, Appl
42	167.5	28.8	417	4	US-08-828-683A-6 Sequence 6, Appli
43	167.5	28.8	428	3	US-08-815-469-2 Sequence 2, Appli
44	166.5	28.6	35	1	US-08-444-005-35 Sequence 35, Appl
45	142	24.4	65	4	US-09-527-236A-24 Sequence 24, Appl

ALIGNMENTS

RESULT 1  
US-08-747-562-37  
; Sequence 37, Application US/08747562  
; Patent No. 6579697  
; GENERAL INFORMATION:  
; APPLICANT: WALLACH, David  
; APPLICANT: BOLDIN, Mark  
; APPLICANT: METT, Igor  
; APPLICANT: VARFOLOMEEV, Eugene  
; TITLE OF INVENTION: MODULATOR OF TNF/NGF SUPERFAMILY RECEPTORS  
; TITLE OF INVENTION: AND SOLUBLE OLIGOMERIC TNF/NGF SUPERFAMILY RECEPTORS  
; NUMBER OF SEQUENCES: 37  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/747,562  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/05854  
; FILING DATE: 11-MAY-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: IL 109,632  
; FILING DATE: 11-MAY-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: IL 111,125  
; FILING DATE: 02-OCT-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWDY, Roger L.  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER: WALLACH=15A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; INFORMATION FOR SEQ ID NO: 37:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 426 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-747-562-37

Query Match 100.0%; Score 582; DB 4; Length 426;  
Best Local Similarity 100.0%; Pred. No. 1.5e-62;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKPSLDTDDPATLYAVVENVPPLRWKEFVRRRLGLSDHEIDRLQLNGRCLREAYSM 60  
Db 316 AHKPSLDTDDPATLYAVVENVPPLRWKEFVRRRLGLSDHEIDRLQLNGRCLREAYSM 375

QY 61 ATWRRTPREATLELLGRVLRMDLLGCLDIEEALCGPAALPPAPSLR 111  
Db 376 ATWRRTPREATLELLGRVLRMDLLGCLDIEEALCGPAALPPAPSLR 426

RESULT 2  
US-09-086-483A-5  
; Sequence 5, Application US/09086483A  
; Patent No. 6214580  
; GENERAL INFORMATION:  
; APPLICANT: NI, et al.  
; TITLE OF INVENTION: HUMAN TUMOR NECROSIS FACTOR RECEPTOR TR10  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.  
; STREET: 9410 KEY WEST AVENUE  
; CITY: ROCKVILLE  
; STATE: MD  
; COUNTRY: US  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/086,483A  
; FILING DATE: May-29-98  
; CLASSIFICATION: 435  
; PRIOR APPLICATION NUMBER: 60/050,936  
; FILING DATE: May-30-97  
; CLASSIFICATION: 435  
; PRIOR APPLICATION NUMBER: 60/069,112  
; FILING DATE: Dec-9-97  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROOKES, ANDERS A.  
; REGISTRATION NUMBER: 36,373  
; REFERENCE/DOCKET NUMBER: PF379  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (301) 309-8504  
; TELEFAX: (301) 309-8439  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 453 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-086-483A-5

Query Match 100.0%; Score 582; DB 3; Length 453;  
Best Local Similarity 100.0%; Pred. No. 1.6e-62;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKPSLDTDDPATLYAVVENVPPLRWKEFVRRRLGLSDHEIDRLQLNGRCLREAYSM 60  
Db 343 AHKPSLDTDDPATLYAVVENVPPLRWKEFVRRRLGLSDHEIDRLQLNGRCLREAYSM 402

QY 61 ATWRRTPREATLELLGRVLRMDLLGCLDIEEALCGPAALPPAPSLR 111  
Db 403 ATWRRTPREATLELLGRVLRMDLLGCLDIEEALCGPAALPPAPSLR 453

RESULT 3  
US-09-580-212-5  
; Sequence 5, Application US/09580212  
; Patent No. 6506569  
; GENERAL INFORMATION:  
; APPLICANT: NI, Jian et al.  
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR10  
; FILE REFERENCE: PF379P1  
; CURRENT APPLICATION NUMBER: US/09/580,212  
; CURRENT FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/136,786  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/142,563  
; PRIOR FILING DATE: 1999-07-07  
; PRIOR APPLICATION NUMBER: 60/144,023  
; PRIOR FILING DATE: 1999-07-15  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 453  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-580-212-5

Query Match 100.0%; Score 582; DB 4; Length 453;  
Best Local Similarity 100.0%; Pred. No. 1.6e-62;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKPSLDTDDPATLYAVVENVPPLRWKEFVRRRLGLSDHEIDRLQLNGRCLREAYSM 60  
Db 343 AHKPSLDTDDPATLYAVVENVPPLRWKEFVRRRLGLSDHEIDRLQLNGRCLREAYSM 402

QY 61 ATWRRTPREATLELLGRVLRMDLLGCLDIEEALCGPAALPPAPSLR 111  
Db 403 ATWRRTPREATLELLGRVLRMDLLGCLDIEEALCGPAALPPAPSLR 453

RESULT 4  
US-09-769-402-5  
; Sequence 5, Application US/09769402  
; Patent No. 6607726  
; GENERAL INFORMATION:  
; APPLICANT: NI, et al.  
; TITLE OF INVENTION: HUMAN TUMOR NECROSIS FACTOR RECEPTOR TR10  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.  
; STREET: 9410 KEY WEST AVENUE  
; CITY: ROCKVILLE  
; STATE: MD  
; COUNTRY: US  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/769,402  
; FILING DATE: 26-Jan-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/086,483  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: 60/069,112  
; FILING DATE: Dec-9-97  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROOKES, ANDERS A.  
; REGISTRATION NUMBER: 36,373  
; REFERENCE/DOCKET NUMBER: PF379  
; TELECOMMUNICATION INFORMATION:



TELEPHONE: (301) 309-8504  
TELEFAX: (301) 309-8439  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 453 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
US-09-769-402-5

Query Match 100.0%; Score 582; DB 4; Length 453;  
Best Local Similarity 100.0%; Pred. No. 1.6e-62;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AHKPSLDTDDPATLYAVVENVPPLRWKEFVRRRLGLSDHEIDRLLELQNGRCLREAYSM 60  
Db 343 AHKPSLDTDDPATLYAVVENVPPLRWKEFVRRRLGLSDHEIDRLLELQNGRCLREAYSM 402  
QY 61 ATWRRTPRREATLELLGRVLRMDLLGCLDIEEALCGPAALPPAPSLR 111  
Db 403 ATWRRTPRREATLELLGRVLRMDLLGCLDIEEALCGPAALPPAPSLR 453

RESULT 5  
US-08-321-668-2  
Sequence 2, Application US/08321668  
Patent No. 5665859  
GENERAL INFORMATION:  
APPLICANT: WALLACH, David  
APPLICANT: BRAKEBUSCH, Cord  
APPLICANT: VARFOLOMEEV, Eugene  
APPLICANT: BATKIN, Michael  
TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING OF  
TITLE OF INVENTION: THE TNF RECEPTORS, THEIR PREPARATION AND THEIR USE  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/321,668  
FILING DATE: 12-OCT-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: IL 107268  
FILING DATE: 12-OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: WALLACH=13  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
TELEX: 248633  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 455 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-321-668-2  
Query Match 100.0%; Score 582; DB 1; Length 455;

Best Local Similarity 100.0%; Pred. No. 1.6e-62;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AHKPSLDTDDPATLYAVVENVPPLRWKEFVRRRLGLSDHEIDRLLELQNGRCLREAYSM 60  
Db 345 AHKPSLDTDDPATLYAVVENVPPLRWKEFVRRRLGLSDHEIDRLLELQNGRCLREAYSM 404  
QY 61 ATWRRTPRREATLELLGRVLRMDLLGCLDIEEALCGPAALPPAPSLR 111  
Db 405 ATWRRTPRREATLELLGRVLRMDLLGCLDIEEALCGPAALPPAPSLR 455

RESULT 6  
US-08-837-941-2  
Sequence 2, Application US/08837941  
Patent No. 5766917  
GENERAL INFORMATION:  
APPLICANT: WALLACH, David  
APPLICANT: BRAKEBUSCH, Cord  
APPLICANT: VARFOLOMEEV, Eugene  
APPLICANT: BATKIN, Michael  
TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING OF  
TITLE OF INVENTION: THE TNF RECEPTORS, THEIR PREPARATION AND THEIR USE  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/837,941  
FILING DATE: 28-APR-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/321,668  
FILING DATE: 12-OCT-1994  
APPLICATION NUMBER: IL 107268  
FILING DATE: 12-OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: WALLACH=13  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
TELEX: 248633  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 455 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-837-941-2

Query Match 100.0%; Score 582; DB 1; Length 455;  
Best Local Similarity 100.0%; Pred. No. 1.6e-62;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AHKPSLDTDDPATLYAVVENVPPLRWKEFVRRRLGLSDHEIDRLLELQNGRCLREAYSM 60  
Db 345 AHKPSLDTDDPATLYAVVENVPPLRWKEFVRRRLGLSDHEIDRLLELQNGRCLREAYSM 404  
QY 61 ATWRRTPRREATLELLGRVLRMDLLGCLDIEEALCGPAALPPAPSLR 111  
Db 405 ATWRRTPRREATLELLGRVLRMDLLGCLDIEEALCGPAALPPAPSLR 455



ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/006,353A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: BROOKES, ANDERS A  
REGISTRATION NUMBER: 36,373  
REFERENCE/DOCKET NUMBER: PF341  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (301) 309-8504  
TELEFAX: (301) 309-8512  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 455 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-006-353A-3

Query Match 100.0%; Score 582; DB 3; Length 455;  
Best Local Similarity 100.0%; Pred. No. 1.6e-62;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKPSLDTDDPATLYAVVENPPLRWKEFVRRGLSDHEIDRLQLNGRCLEAQSML 60

Db 345 AHKPSLDTDDPATLYAVVENPPLRWKEFVRRGLSDHEIDRLQLNGRCLEAQSML 404

QY 61 ATWRRTPRREATLELLGRVLRDMDLLGCLIEDIEALCGPAALPPAPSLR 111

Db 405 ATWRRTPRREATLELLGRVLRDMDLLGCLIEDIEALCGPAALPPAPSLR 455

RESULT 10

US-09-527-236A-5  
Sequence 5, Application US/09527236A  
Patent No. 6358508  
GENERAL INFORMATION:  
APPLICANT: Ni, Jian  
APPLICANT: Yu, Guo-Liang  
APPLICANT: Fan, Ping  
APPLICANT: Gentz, Reiner L.  
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9  
FILE REFERENCE: PF375P1  
CURRENT APPLICATION NUMBER: US/09/527,236A  
CURRENT FILING DATE: 2000-03-16  
PRIOR APPLICATION NUMBER: 60/052,991  
PRIOR FILING DATE: 1997-06-11  
PRIOR APPLICATION NUMBER: 09/095,094  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/126,019  
PRIOR FILING DATE: 1999-03-24  
PRIOR APPLICATION NUMBER: 60/134,220  
PRIOR FILING DATE: 1999-05-14  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 5  
LENGTH: 455  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-527-236A-5

Query Match 100.0%; Score 582; DB 4; Length 455;  
Best Local Similarity 100.0%; Pred. No. 1.6e-62;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKPSLDTDDPATLYAVVENPPLRWKEFVRRGLSDHEIDRLQLNGRCLEAQSML 60

Db 345 AHKPSLDTDDPATLYAVVENPPLRWKEFVRRGLSDHEIDRLQLNGRCLEAQSML 404

QY 61 ATWRRTPRREATLELLGRVLRDMDLLGCLIEDIEALCGPAALPPAPSLR 111

Db 405 ATWRRTPRREATLELLGRVLRDMDLLGCLIEDIEALCGPAALPPAPSLR 455

RESULT 11

US-08-054-970-2  
Sequence 2, Application US/08054970  
Patent No. 6395267  
GENERAL INFORMATION:  
APPLICANT: WALLACH, David  
APPLICANT: BRAKEBUSCH, Cord  
TITLE OF INVENTION: TNF RECEPTOR ACTION MODULATION  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/054,970  
FILING DATE: 03-MAY-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Townsend, Kevin G.  
REGISTRATION NUMBER: 34,033  
REFERENCE/DOCKET NUMBER: WALLACH=9  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
TELEX: 248633  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 455 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-054-970-2

Query Match 100.0%; Score 582; DB 4; Length 455;  
Best Local Similarity 100.0%; Pred. No. 1.6e-62;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKPSLDTDDPATLYAVVENPPLRWKEFVRRGLSDHEIDRLQLNGRCLEAQSML 60

Db 345 AHKPSLDTDDPATLYAVVENPPLRWKEFVRRGLSDHEIDRLQLNGRCLEAQSML 404

QY 61 ATWRRTPRREATLELLGRVLRDMDLLGCLIEDIEALCGPAALPPAPSLR 111

Db 405 ATWRRTPRREATLELLGRVLRDMDLLGCLIEDIEALCGPAALPPAPSLR 455

RESULT 12

US-09-565-918-4  
Sequence 4, Application US/09565918  
Patent No. 6433147  
GENERAL INFORMATION:  
APPLICANT: Ni, Jian  
APPLICANT: Rosen, Craig A.  
APPLICANT: Pan, James G.  
APPLICANT: Gentz, Reiner L.  
APPLICANT: Dixit, Vishva M.  
TITLE OF INVENTION: Death Domain Containing Receptor 4

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; FILE REFERENCE: 1488.1300005
; CURRENT APPLICATION NUMBER: US/09/565,918
; CURRENT FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: US 60/132,922
; PRIOR FILING DATE: 1999-05-06
; PRIOR APPLICATION NUMBER: US 09/013,895
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: US 60/037,829
; PRIOR FILING DATE: 1997-02-05
; PRIOR APPLICATION NUMBER: US 60/035,722
; PRIOR FILING DATE: 1997-01-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-565-918-4

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Best Local Similarity 100.0%; Pred. No. 1.6e-62;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AHKPQSLDTPATLYAVVENVPPLRWKEFVRRRLGSLDHEIDRLQLONGRCLREAQYSML 60
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QY      61 ATWRRRTPRREATLELLGRVLRDMDLLGCLDIEEALCGPAALPPAPSLLR 111
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RESULT 13
US-09-573-986-3
; Sequence 3, Application US/09573986
; Patent No. 6455040
; GENERAL INFORMATION:
; APPLICANT: Wei, Ying-Fei
; APPLICANT: Ni, Jian
; APPLICANT: Gentz, Reiner
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
; FILE REFERENCE: 1488.1280004
; CURRENT APPLICATION NUMBER: US/09/573,986
; CURRENT FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-573-986-3

Query Match      100.0%; Score 582; DB 4; Length 455;
Best Local Similarity 100.0%; Pred. No. 1.6e-62;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AHKPQSLDTPATLYAVVENVPPLRWKEFVRRRLGSLDHEIDRLQLONGRCLREAQYSML 60
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RESULT 14
US-09-027-287-3
; Sequence 3, Application US/09027287A
; Patent No. 6479254
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; APPLICANT: Yu, Guo-Liang
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; APPLICANT: Ruben, Steven M.
; APPLICANT: Ullrich, Stephen
; TITLE OF INVENTION: Apoptosis Inducing Molecule II
; FILE REFERENCE: 1488.0650004
; CURRENT APPLICATION NUMBER: US/09/027,287A
; CURRENT FILING DATE: 1998-02-20
; EARLIER APPLICATION NUMBER: US 09/003,886
; EARLIER FILING DATE: 1998-01-07
; EARLIER APPLICATION NUMBER: US 08/822,953
; EARLIER FILING DATE: 1997-03-21
; EARLIER APPLICATION NUMBER: US 60/030,157
; EARLIER FILING DATE: 1996-10-31
; EARLIER APPLICATION NUMBER: US 60/013,923
; EARLIER FILING DATE: 1996-03-22
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.0
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; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-027-287-3

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Best Local Similarity 100.0%; Pred. No. 1.6e-62;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      61 ATWRRRTPRREATLELLGRVLRDMDLLGCLDIEEALCGPAALPPAPSLLR 111
Db      405 ATWRRRTPRREATLELLGRVLRDMDLLGCLDIEEALCGPAALPPAPSLLR 455

RESULT 15
US-09-252-656B-3
; Sequence 3, Application US/09252656B
; Patent No. 6495520
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ruben, Steven M.
; APPLICANT: Zhang, Jun
; APPLICANT: Ullrich, Stephen
; APPLICANT: Zhai, Yifan
; TITLE OF INVENTION: Apoptosis Inducing Molecule II and Methods of Use
; FILE REFERENCE: 1488.0650006
; CURRENT APPLICATION NUMBER: US/09/252,656B
; CURRENT FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: US 60/075,409
; PRIOR FILING DATE: 1998-02-20
; PRIOR APPLICATION NUMBER: US 09/027,287
; PRIOR FILING DATE: 1998-02-20
; PRIOR APPLICATION NUMBER: US 09/003,886
; PRIOR FILING DATE: 1998-01-07
; PRIOR APPLICATION NUMBER: US 08/822,953
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/013,923
; PRIOR FILING DATE: 1996-03-22
; PRIOR APPLICATION NUMBER: US 60/030,157
; PRIOR FILING DATE: 1996-10-31
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-252-656B-3

Query Match      100.0%; Score 582; DB 4; Length 455;
Best Local Similarity 100.0%; Pred. No. 1.6e-62;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Job time : 13.9581 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 1, 2004, 14:43:57 ; Search time 35.8922 Seconds  
(without alignments)  
863.605 Million cell updates/sec

Title: US-09-854-906-8  
Perfect score: 582  
Sequence: 1 AHKPQSLDTPATLYAVVE.....DIEALCGPAALPPAPSLR 111

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Gapop 10.0 , Gapext 0.5

Searched: 1151071 seqs, 279249464 residues

Total number of hits satisfying chosen parameters: 1151071

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:  
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18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	582	100.0	158	14	US-10-043-487-301 Sequence 301, App
2	582	100.0	426	15	US-10-349-977-37 Sequence 37, Appl
3	582	100.0	453	14	US-10-280-047-5 Sequence 5, Appli
4	582	100.0	455	9	US-09-826-212-3 Sequence 3, Appli
5	582	100.0	455	9	US-09-333-966-5 Sequence 5, Appli
6	582	100.0	455	9	US-09-027-287-3 Sequence 3, Appli
7	582	100.0	455	9	US-09-874-138-3 Sequence 3, Appli
8	582	100.0	455	9	US-09-840-707A-16 Sequence 16, Appl
9	582	100.0	455	9	US-09-252-656B-3 Sequence 3, Appli
10	582	100.0	455	9	US-09-899-422-2 Sequence 2, Appli
11	582	100.0	455	9	US-09-899-422-17 Sequence 17, Appl
12	582	100.0	455	9	US-09-935-727-5 Sequence 5, Appli
13	582	100.0	455	9	US-09-898-234-2 Sequence 2, Appli
14	582	100.0	455	9	US-09-898-234-17 Sequence 17, Appl
15	582	100.0	455	9	US-09-756-854-5 Sequence 5, Appli

16	582	100.0	455	9	US-09-899-429A-2	Sequence 2, Appli
17	582	100.0	455	9	US-09-899-429A-27	Sequence 27, Appl
18	582	100.0	455	9	US-09-792-356-2	Sequence 2, Appli
19	582	100.0	455	9	US-09-792-356-17	Sequence 17, Appl
20	582	100.0	455	10	US-09-314-889-5	Sequence 5, Appli
21	582	100.0	455	10	US-09-945-505-3	Sequence 3, Appli
22	582	100.0	455	12	US-10-099-007A-13	Sequence 13, Appl
23	582	100.0	455	13	US-10-005-842-3	Sequence 3, Appli
24	582	100.0	455	13	US-10-120-397-2	Sequence 2, Appli
25	582	100.0	455	13	US-10-041-574-5	Sequence 5, Appli
26	582	100.0	455	14	US-10-252-408-4	Sequence 4, Appli
27	582	100.0	455	14	US-10-038-557A-16	Sequence 16, Appl
28	582	100.0	455	14	US-10-175-902-4	Sequence 4, Appli
29	582	100.0	455	14	US-10-186-643-3	Sequence 3, Appli
30	582	100.0	455	14	US-10-189-189-5	Sequence 5, Appli
31	582	100.0	455	15	US-10-375-680-3	Sequence 3, Appli
32	582	100.0	455	15	US-10-418-242-5	Sequence 5, Appli
33	582	100.0	455	15	US-10-440-464-59	Sequence 59, Appl
34	582	100.0	909	14	US-10-226-296-4	Sequence 4, Appli
35	582	100.0	909	14	US-10-226-318-4	Sequence 2, Appli
36	424	72.9	471	9	US-09-970-532-2	Sequence 2, Appli
37	407	69.9	78	9	US-09-887-879-16	Sequence 16, Appl
38	407	69.9	78	9	US-09-992-964-16	Sequence 16, Appl
39	407	69.9	78	12	US-10-207-295-10	Sequence 10, Appl
40	407	69.9	78	13	US-10-112-793-23	Sequence 23, Appl
41	407	69.9	78	14	US-10-242-383-16	Sequence 16, Appl
42	386	66.3	461	9	US-09-899-422-15	Sequence 15, Appl
43	386	66.3	461	9	US-09-898-234-15	Sequence 15, Appl
44	386	66.3	461	9	US-09-899-429A-25	Sequence 25, Appl
45	386	66.3	461	9	US-09-792-356-15	Sequence 15, Appl

ALIGNMENTS

RESULT 1  
US-10-043-487-301  
; Sequence 301, Application US/10043487  
; Publication No. US20030055220A1  
; GENERAL INFORMATION:  
; APPLICANT: HYBRIGENICS  
; APPLICANT: Pierre, LEGRAIN  
; TITLE OF INVENTION: Protein-protein interactions between Shigella Flexneri polypeptid  
; TITLE OF INVENTION: mammalian polypeptides  
; FILE REFERENCE: B4778A  
; CURRENT APPLICATION NUMBER: US/10/043,487  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/261,130  
; PRIOR FILING DATE: 2001-01-12  
; NUMBER OF SEQ ID NOS: 561  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 301  
; LENGTH: 158  
; TYPE: PRT  
; ORGANISM: Shigella Flexneri  
US-10-043-487-301

Query Match 100.0%; Score 582; DB 14; Length 158;  
Best Local Similarity 100.0%; Pred. No. 1.8e-58;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2  
US-10-349-977-37  
; Sequence 37, Application US/10349977

Publication No. US20040013646A1  
GENERAL INFORMATION:  
APPLICANT: WALLACH, David  
BOLDIN, Mark  
METT, Igor  
VARFOLOMEEV, Eugene  
TITLE OF INVENTION: MODULATOR OF TNF/NGF SUPERFAMILY RECEPTORS  
AND SOLUBLE OLIGOMERIC TNF/NGF SUPERFAMILY RECEPTORS  
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/349,977  
FILING DATE: 24-Jan-2003  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/747,562  
FILING DATE: 11-MAY-1995  
APPLICATION NUMBER: PCT/US95/05854  
FILING DATE: 11-MAY-1994  
APPLICATION NUMBER: IL 109,632  
FILING DATE: 02-OCT-1994  
APPLICATION NUMBER: IL 111,125  
FILING DATE: 02-OCT-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: WALLACH=15A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 426 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 37:  
US-10-349-977-37  
Query Match 100.0%; Score 582; DB 15; Length 426;  
Best Local Similarity 100.0%; Pred. No. 5.8e-58;  
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RESULT 3  
US-10-280-047-5  
Sequence 5, Application US/10280047  
Publication No. US20030180883A1  
GENERAL INFORMATION:  
APPLICANT: Ni, Jian  
APPLICANT: Rosen, Craig A  
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor 10  
FILE REFERENCE: PF379PID1  
CURRENT APPLICATION NUMBER: US/10/280,047

CURRENT FILING DATE: 2002-10-25  
PRIOR APPLICATION NUMBER: 09/580,212  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: 09/086,483  
PRIOR FILING DATE: 1998-05-29  
PRIOR APPLICATION NUMBER: 60/069,112  
PRIOR FILING DATE: 1997-12-09  
PRIOR APPLICATION NUMBER: 60/050,936  
PRIOR FILING DATE: 1997-05-30  
PRIOR APPLICATION NUMBER: 60/144,023  
PRIOR FILING DATE: 1999-07-15  
PRIOR APPLICATION NUMBER: 60/142,563  
PRIOR FILING DATE: 1999-07-07  
PRIOR APPLICATION NUMBER: 60/136,786  
PRIOR FILING DATE: 1999-05-28  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 5  
LENGTH: 453  
TYPE: PRT  
ORGANISM: human  
US-10-280-047-5  
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Best Local Similarity 100.0%; Pred. No. 6.3e-58;  
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QY 61 ATWRRRTPRREATLELLGRVLRDMDLLGCLEDIEEALCGPAALPPAPSLLR 111  
Db 403 ATWRRRTPRREATLELLGRVLRDMDLLGCLEDIEEALCGPAALPPAPSLLR 453  
RESULT 4  
US-09-826-212-3  
Sequence 3, Application US/09826212  
Patent No. US20010021516A1  
GENERAL INFORMATION:  
APPLICANT: Wei, Ying-Fei  
APPLICANT: Gentz, Reiner  
APPLICANT: Ruben, Steven  
APPLICANT: Ni, Jian  
TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5  
FILE REFERENCE: 1488.1280006  
CURRENT APPLICATION NUMBER: US/09/826,212  
CURRENT FILING DATE: 2001-04-05  
NUMBER OF SEQ ID NOS: 26  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 3  
LENGTH: 455  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-826-212-3  
Query Match 100.0%; Score 582; DB 9; Length 455;  
Best Local Similarity 100.0%; Pred. No. 6.3e-58;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AHKPSLDTDDPATLYAVVENVPLRWKEFVRRRLGLSDHEIDRLLELQNGRCLREAQYSML 60  
Db 345 AHKPSLDTDDPATLYAVVENVPLRWKEFVRRRLGLSDHEIDRLLELQNGRCLREAQYSML 404  
QY 61 ATWRRRTPRREATLELLGRVLRDMDLLGCLEDIEEALCGPAALPPAPSLLR 111  
Db 405 ATWRRRTPRREATLELLGRVLRDMDLLGCLEDIEEALCGPAALPPAPSLLR 455  
RESULT 5  
US-09-333-966-5  
Sequence 5, Application US/09333966

Patent No. US20020009773A1  
; GENERAL INFORMATION:  
; APPLICANT: Yu, Guo-Liang  
; APPLICANT: Ni, Jian  
; APPLICANT: Dixit, Vishva  
; APPLICANT: Gentz, Reiner L.  
; APPLICANT: Dillon, Patrick J.  
; TITLE OF INVENTION: Death Domain Containing Receptors  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.  
; STREET: 1100 New York Ave., NW, Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/333,966  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/815,469  
; FILING DATE:  
; APPLICATION NUMBER: No. US20020009773A1 Yet Assigned  
; FILING DATE: 06-FEB-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/028,711  
; FILING DATE: 17-OCT-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/013,285  
; FILING DATE: 12-MAR-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Steffe, Eric K.  
; REGISTRATION NUMBER: 36,688  
; REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 455 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: No. US20020009773A1 Relevant  
; TOPOLOGY: No. US20020009773A1 Relevant  
; MOLECULE TYPE: protein  
; US-09-333-966-5  
  
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Best Local Similarity 100.0%; Pred. No. 6.3e-58;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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Db 345 AHKPSLDTDDPATLYAVVENVPPLRWKEFVRRGLSDHEIDRLQLNGRCLREAQYSML 404  
  
QY 61 ATWRRTPRREATLELLGRVLRMDLLGCLDEIEALCGPAALPPAPSLR 111  
Db 405 ATWRRTPRREATLELLGRVLRMDLLGCLDEIEALCGPAALPPAPSLR 455  
  
RESULT 6  
US-09-027-287-3  
; Sequence 3, Application US/09027287A  
; Patent No. US20020064869A1  
; GENERAL INFORMATION:  
; APPLICANT: Ebner, Reinhard  
; APPLICANT: Yu, Guo-Liang  
; APPLICANT: Ruben, Steven M.

APPLICANT: Ullrich, Stephen  
; TITLE OF INVENTION: Apoptosis Inducing Molecule II  
; FILE REFERENCE: 1488.0650004  
; CURRENT APPLICATION NUMBER: US/09/027,287A  
; CURRENT FILING DATE: 1998-02-20  
; EARLIER APPLICATION NUMBER: US 09/003,886  
; EARLIER FILING DATE: 1998-01-07  
; EARLIER APPLICATION NUMBER: US 08/822,953  
; EARLIER FILING DATE: 1997-03-21  
; EARLIER APPLICATION NUMBER: US 60/030,157  
; EARLIER FILING DATE: 1996-10-31  
; EARLIER APPLICATION NUMBER: US 60/013,923  
; EARLIER FILING DATE: 1996-03-22  
; NUMBER OF SEQ ID NOS: 55  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 455  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-027-287-3  
  
Query Match 100.0%; Score 582; DB 9; Length 455;  
Best Local Similarity 100.0%; Pred. No. 6.3e-58;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 AHKPSLDTDDPATLYAVVENVPPLRWKEFVRRGLSDHEIDRLQLNGRCLREAQYSML 60  
Db 345 AHKPSLDTDDPATLYAVVENVPPLRWKEFVRRGLSDHEIDRLQLNGRCLREAQYSML 404  
  
QY 61 ATWRRTPRREATLELLGRVLRMDLLGCLDEIEALCGPAALPPAPSLR 111  
Db 405 ATWRRTPRREATLELLGRVLRMDLLGCLDEIEALCGPAALPPAPSLR 455  
  
RESULT 7  
US-09-874-138-3  
; Sequence 3, Application US/09874138  
; Patent No. US20020072091A1  
; GENERAL INFORMATION:  
; APPLICANT: Ni, Jian  
; APPLICANT: Gentz, Reiner L.  
; APPLICANT: Yu, Guo-liang  
; APPLICANT: Rosen, Craig A.  
; TITLE OF INVENTION: Death Domain Containing Receptor 5  
; FILE REFERENCE: 1488.1310006  
; CURRENT APPLICATION NUMBER: US/09/874,138  
; CURRENT FILING DATE: 2001-06-06  
; PRIOR APPLICATION NUMBER: 09/565,009  
; PRIOR FILING DATE: 2000-05-04  
; PRIOR APPLICATION NUMBER: 60/148,939  
; PRIOR FILING DATE: 1999-08-13  
; PRIOR APPLICATION NUMBER: 60/133,238  
; PRIOR FILING DATE: 1999-05-07  
; PRIOR APPLICATION NUMBER: 60/132,498  
; PRIOR FILING DATE: 1999-05-04  
; PRIOR APPLICATION NUMBER: 09/042,583  
; PRIOR FILING DATE: 1998-03-17  
; PRIOR APPLICATION NUMBER: 60/054,021  
; PRIOR FILING DATE: 1997-07-29  
; PRIOR APPLICATION NUMBER: 60/040,846  
; PRIOR FILING DATE: 1997-03-17  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 455  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-874-138-3  
  
Query Match 100.0%; Score 582; DB 9; Length 455;  
Best Local Similarity 100.0%; Pred. No. 6.3e-58;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



[illegible]

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RESULT 8
US-09-840-707A-16
; Sequence 16, Application US/09840707A
; Patent No. US20020077276A1
; GENERAL INFORMATION:
; APPLICANT: Fredeking, Terry M.
; APPLICANT: Ignatyev, George M.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING HEMORRHAGIC VIRUS
; TITLE OF INVENTION: INFECTIONS AND OTHER DISORDERS
; FILE REFERENCE: 24881-301C
; CURRENT APPLICATION NUMBER: US/09/840,707A
; CURRENT FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: 09/562,979
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/198,210
; PRIOR FILING DATE: 1999-04-27
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Tumor Necrosis Factor p55 Receptor
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AAA36753/GenBank
; DATABASE ENTRY DATE: 1995-08-03
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US-09-840-707A-16

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	Best Local Similarity	100.0%;	Pred. No. 6.3e-58;					
	Matches 111;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;			
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Db	345	AHKPQSLD	TD	PATLYAV	VNPPLRWKEFVRR	GLSDHEIDRLQLNGRCL	REAQYSML	404
QY	61	ATWRRRT	PR	REATLE	LLGRVLRDMDLL	GCLEDIEEALCGPAAL	PAPSLLR	111
Db	405	ATWRRRT	PR	REATLE	LLGRVLRDMDLL	GCLEDIEEALCGPAAL	PAPSLLR	455

RESULT 9  
US-09-252-656B-3  
; Sequence 3, Application US/09252656B  
; Patent No. US20020081647A1  
; GENERAL INFORMATION:  
; APPLICANT: Ebner, Reinhard  
; APPLICANT: Yu, Guo-Liang  
; APPLICANT: Ruben, Steven M.  
; APPLICANT: Zhang, Jun  
; APPLICANT: Ullrich, Stephen  
; APPLICANT: Zhai, Yifan  
; TITLE OF INVENTION: Apoptosis Inducing Molecule II and Methods of Use  
; FILE REFERENCE: 1488.0650006  
; CURRENT APPLICATION NUMBER: US/09/252,656B  
; CURRENT FILING DATE: 1999-02-19  
; PRIOR APPLICATION NUMBER: US 60/075,409  
; PRIOR FILING DATE: 1998-02-20  
; PRIOR APPLICATION NUMBER: US 09/027,287  
; PRIOR FILING DATE: 1998-02-20  
; PRIOR APPLICATION NUMBER: US 09/003,886  
; PRIOR FILING DATE: 1998-01-07  
; PRIOR APPLICATION NUMBER: US 08/822,953

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; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/013,923
; PRIOR FILING DATE: 1996-03-22
; PRIOR APPLICATION NUMBER: US 60/030,157
; PRIOR FILING DATE: 1996-10-31
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
;   LENGTH: 455
;   TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-252-656B-3

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	Query Match	100.0%;	Score 582;	DB 9;	Length 455;
	Best Local Similarity	100.0%;	Pred. No. 6.3e-58;		
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Dd	345	AHKPQSLDTPATLYAVVENVPPLRWKEFVRRLGLSDHEIDRLLELQNGRCILREAAQYSML	404		
QY	61	ATWRRRTPREATLELLGRVLRDMDLGCLDIEEALCGPAALPPAPPSLLR	111		
pB	405	ATWRRRTPREATLELLGRVLRDMDLGCLDIEEALCGPAALPPAPPSLLE	455		

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RESULT 10
US-09-899-422-2
; Sequence 2, Application US/09899422
; Patent No. US2002090676A1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
; APPLICANT: Himmler, Adolph
; APPLICANT: Maurer-Fogy, Ingrid
; APPLICANT: Stratowa, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
; TITLE OF INVENTION: Them
; FILE REFERENCE: 98,385-H
; CURRENT APPLICATION NUMBER: US/09/899,422
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 09/525,998
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 08/383,676
; PRIOR FILING DATE: 1995-02-01
; PRIOR APPLICATION NUMBER: 08/153,287
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: 07/821,750
; PRIOR FILING DATE: 1992-01-02
; PRIOR APPLICATION NUMBER: 07/511,430
; PRIOR FILING DATE: 1990-04-20
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
;
US-09-899-422-2

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	Query Match	100.0%;	Score 582;	DB 9;	Length 455;
	Best Local Similarity	100.0%;	Pred. No. 6.3e-58;		
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Dd	345 AHKPSLDTDDPATLYAVVENVPLRWKEFVRRLGLSDHEIDRLQLONGRCLREAQYSML	404			
Qy	61 AIWRRRTPRREATLELLGRVLRDMDLLGLEDIEEALCGPAALPPAPSLLR	111			
Dd	405 ATWDPTTDPREACTIETIGRVIRDMDLGGLEDIEEALCGPAALPPAPSLLR	455			

RESULT 11  
US-09-899-422-17

; Sequence 17, Application US/09899422  
; Patent No. US20020090676A1  
; GENERAL INFORMATION:  
; APPLICANT: Hauptmann, Rudolph  
; APPLICANT: Himmeler, Adolph  
; APPLICANT: Maurer-Fogy, Ingrid  
; APPLICANT: Stratowa, Christian  
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for  
; FILE REFERENCE: 98,385-H  
; CURRENT APPLICATION NUMBER: US/09/899,422  
; CURRENT FILING DATE: 2001-08-21  
; PRIOR APPLICATION NUMBER: 09/525,998  
; PRIOR FILING DATE: 2000-03-15  
; PRIOR APPLICATION NUMBER: 08/383,676  
; PRIOR FILING DATE: 1995-02-01  
; PRIOR APPLICATION NUMBER: 08/153,287  
; PRIOR FILING DATE: 1993-11-17  
; PRIOR APPLICATION NUMBER: 07/821,750  
; PRIOR FILING DATE: 1992-01-02  
; PRIOR APPLICATION NUMBER: 07/511,430  
; PRIOR FILING DATE: 1990-04-20  
; NUMBER OF SEQ ID NOS: 87  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 17  
; LENGTH: 455  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: human TNF-R in  
; OTHER INFORMATION: lTNF-R2  
US-09-899-422-17

Query Match 100.0%; Score 582; DB 9; Length 455;  
Best Local Similarity 100.0%; Pred. No. 6.3e-58;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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Db 345 AHKPSLDTDDPATLYAVVENVPPLRWKEFVRRRLGSLDHEIDRLQLNGRCLREAQYSML 404  
  
QY 61 ATWRRTPRREATLELLGRVLRDMDLLGCLEDEIEEALCGPAALPPAPSLLR 111  
Db 405 ATWRRTPRREATLELLGRVLRDMDLLGCLEDEIEEALCGPAALPPAPSLLR 455

RESULT 12  
US-09-935-727-5  
; Sequence 5, Application US/09935727  
; Patent No. US20020150583A1  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta  
; FILE REFERENCE: PF454P2  
; CURRENT APPLICATION NUMBER: US/09/935,727  
; CURRENT FILING DATE: 2001-08-24  
; PRIOR APPLICATION NUMBER: 60/303,224  
; PRIOR FILING DATE: 2001-07-06  
; PRIOR APPLICATION NUMBER: 60/252,131  
; PRIOR FILING DATE: 2000-11-21  
; PRIOR APPLICATION NUMBER: 60/227,598  
; PRIOR FILING DATE: 2000-08-25  
; PRIOR APPLICATION NUMBER: 09/518,931  
; PRIOR FILING DATE: 2000-03-03  
; PRIOR APPLICATION NUMBER: 60/168,235  
; PRIOR FILING DATE: 1999-12-01  
; PRIOR APPLICATION NUMBER: 60/146,371  
; PRIOR FILING DATE: 1999-08-02  
; PRIOR APPLICATION NUMBER: 60/131,964  
; PRIOR FILING DATE: 1999-04-30  
; PRIOR APPLICATION NUMBER: 60/131,270  
; PRIOR FILING DATE: 1999-04-27  
; PRIOR APPLICATION NUMBER: 60/124,092

; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/121,774  
; PRIOR FILING DATE: 1999-03-04  
; PRIOR APPLICATION NUMBER: 09/006,352  
; PRIOR FILING DATE: 1998-01-13  
; PRIOR APPLICATION NUMBER: 60/035,496  
; PRIOR FILING DATE: 1997-01-14  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 455  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-935-727-5

Query Match 100.0%; Score 582; DB 9; Length 455;  
Best Local Similarity 100.0%; Pred. No. 6.3e-58;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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Db 345 AHKPSLDTDDPATLYAVVENVPPLRWKEFVRRRLGSLDHEIDRLQLNGRCLREAQYSML 404  
  
QY 61 ATWRRTPRREATLELLGRVLRDMDLLGCLEDEIEEALCGPAALPPAPSLLR 111  
Db 405 ATWRRTPRREATLELLGRVLRDMDLLGCLEDEIEEALCGPAALPPAPSLLR 455

RESULT 13  
US-09-898-234-2  
; Sequence 2, Application US/09898234  
; Patent No. US20020155112A1  
; GENERAL INFORMATION:  
; APPLICANT: Hauptmann, Rudolph  
; APPLICANT: Himmeler, Adolph  
; APPLICANT: Maurer-Fogy, Ingrid  
; APPLICANT: Stratowa, Christian  
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for  
; FILE REFERENCE: 98,385-I  
; CURRENT APPLICATION NUMBER: US/09/898,234  
; CURRENT FILING DATE: 2001-07-03  
; PRIOR APPLICATION NUMBER: 09/525,998  
; PRIOR FILING DATE: 2000-03-15  
; PRIOR APPLICATION NUMBER: 08/383,676  
; PRIOR FILING DATE: 1995-02-01  
; PRIOR APPLICATION NUMBER: 08/153,287  
; PRIOR FILING DATE: 1993-11-17  
; PRIOR APPLICATION NUMBER: 07/821,750  
; PRIOR FILING DATE: 1992-01-02  
; PRIOR APPLICATION NUMBER: 07/511,430  
; PRIOR FILING DATE: 1990-04-20  
; NUMBER OF SEQ ID NOS: 87  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 455  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-898-234-2

Query Match 100.0%; Score 582; DB 9; Length 455;  
Best Local Similarity 100.0%; Pred. No. 6.3e-58;  
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Db 345 AHKPSLDTDDPATLYAVVENVPPLRWKEFVRRRLGSLDHEIDRLQLNGRCLREAQYSML 404  
  
QY 61 ATWRRTPRREATLELLGRVLRDMDLLGCLEDEIEEALCGPAALPPAPSLLR 111  
Db 405 ATWRRTPRREATLELLGRVLRDMDLLGCLEDEIEEALCGPAALPPAPSLLR 455



GenCore version 5.1.6  
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OM protein - protein search, using sw model

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(without alignments)  
917.942 Million cell updates/sec

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Perfect score: 582  
Sequence: 1 AHKPQSLDTPATLYAVVE.....DIEEALCGPAALPPAPSLLR 111

Scoring table: BLOSUM62  
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Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 78:\*  
1: Pirl:\*  
2: Pirl2:\*  
3: Pirl3:\*  
4: Pirl4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	462.5	79.5	461	2 JC4302	tumor necrosis fac
3	386	66.3	461	1 GQRTT1	tumor necrosis fac
4	350.5	60.2	454	1 GQGST1	tumor necrosis fac
5	91.5	15.7	671	2 T09479	serine/threonine p
6	90	15.5	656	2 I49299	receptor interacti
7	86	14.8	1848	2 S37771	ankyrin, erythrocy
8	86	14.8	1862	2 I49502	ankyrin - mouse
9	82	14.1	163	2 B72550	probable methylmal
10	80.5	13.8	1765	2 T42714	ankyrin 3, splice
11	80.5	13.8	1940	2 T42715	ankyrin 3, splice
12	80.5	13.8	1943	2 T42713	ankyrin 3, splice
13	80.5	13.8	1961	2 T42716	ankyrin 3, splice
14	80.5	13.8	4377	2 A55575	ankyrin 3, long sp
15	80	13.7	1856	2 B35049	ankyrin 1, erythro
16	80	13.7	1880	2 A35049	ankyrin 1, erythro
17	80	13.7	1881	1 SJHUK	ankyrin 1, erythro
18	78.5	13.5	388	2 E95177	aminotransferase,
19	77.5	13.3	591	2 T41531	activator of Hsp70
20	77.5	13.3	591	2 T51996	hypothetical prote
21	77	13.2	316	2 D83192	acetyl-coenzyme A
22	75.5	13.0	138	2 S37773	ankyrin, erythrocy
23	74.5	12.8	208	2 A56912	FADD protein - hum
24	74.5	12.8	388	2 G98043	aminotransferase (
25	74.5	12.8	426	2 I48379	gene hb protein -
26	74.5	12.8	3924	2 S37431	ankyrin 2, neurona
27	74	12.7	536	2 D83419	probable ATP-bindi
28	72.5	12.5	295	2 A86745	conserved hypothet
29	72.5	12.5	580	2 G82693	glutaminyl-tRNA sy

30	72	12.4	585	2	C49596	genome polyprotein
31	71.5	12.3	192	2	T30477	hypothetical prote
32	71.5	12.3	902	2	A55543	cmaa protein - Pse
33	71	12.2	812	2	A83379	glycogen phosphory
34	70.5	12.1	402	2	E71279	hypothetical prote
35	70	12.0	643	2	E83142	probable transcrip
36	69.5	11.9	412	2	E88736	protein F33D4.6a l
37	69.5	11.9	446	2	AD3460	UDP-N-acetylglucos
38	69.5	11.9	529	2	F84106	hypothetical prote
39	69.5	11.9	672	2	T32557	hypothetical prote
40	69.5	11.9	1805	2	A34736	nestin - rat
41	69	11.9	481	2	I51567	tryptophan 5-monoo
42	69	11.9	533	2	G75348	conserved hypothet
43	69	11.9	1438	2	T17402	dihydroaeruginoinc
44	69	11.9	1548	2	T04456	hypothetical prote
45	69	11.9	1882	1	GNVVTR	genome polyprotein

ALIGNMENTS

RESULT 1

GQHUT1

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N;Alternate names: P55 tumor necrosis factor receptor; TNF receptor type 1  
N;Contains: tumor necrosis factor alpha inhibitor; tumor necrosis factor binding proteir  
C;Species: Homo sapiens (man)  
C;Date: 30-Jun-1992 #sequence revision 30-Jun-1992 #text change 08-Dec-2000  
C;Accession: A38208; A34899; A34900; A36555; C36555; A38281; S12057; JT0758; A60231; A38  
R;Fuchs, P.; Strehl, S.; Dworzak, M.; Himmler, A.; Ambros, P.F.  
Genomics 13, 219-224, 1992  
A;Title: Structure of the human TNF receptor 1 (p60) gene (TNRF1) and localization to ch  
A;Reference number: A38208; MUID:92250049; PMID:1315717  
A;Accession: A38208  
A;Molecule type: DNA  
A;Residues: 1-455 <FUC>  
A;Cross-references: GB:M75864; GB:M75865; GB:M75866; NID:g339748; PIDN:AAA61201.1; PID:g  
R;Loetscher, H.; Pan, Y.C.E.; Lahm, H.W.; Gentz, R.; Brockhaus, M.; Tabuchi, H.; Lesslau  
Cell 61, 351-359, 1990  
A;Title: Molecular cloning and expression of the human 55 kd tumor necrosis factor recep  
A;Reference number: A34899; MUID:90235284; PMID:2158862  
A;Accession: A34899  
A;Molecule type: mRNA  
A;Residues: 1-455 <LOE>  
A;Cross-references: GB:M58286; GB:M33480; NID:g339753; PIDN:AAA36753.1; PID:g339754  
A;Experimental source: Placenta  
A;Note: part of this sequence, including the amino end of the mature protein, confirmed  
R;Schall, T.J.; Lewis, M.; Koller, K.J.; Lee, A.; Rice, G.C.; Wong, G.H.W.; Gatanaga, T.  
Cell 61, 361-370, 1990  
A;Title: Molecular cloning and expression of a receptor for human tumor necrosis factor.  
A;Reference number: A34900; MUID:90235285; PMID:2158863  
A;Accession: A34900  
A;Molecule type: mRNA  
A;Residues: 1-455 <SCH>  
A;Cross-references: GB:M33294; NID:g339744; PIDN:AAA03210.1; PID:g339745  
R;Himmler, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.; Pfizenmaier, K.; Lantz, M.;  
DNA Cell Biol. 9, 705-715, 1990  
A;Title: Molecular cloning and expression of human and rat tumor necrosis factor recepto  
A;Reference number: A36555; MUID:91090841; PMID:1702293  
A;Accession: A36555  
A;Molecule type: mRNA  
A;Residues: 1-455 <HIM>  
A;Cross-references: GB:M63121; NID:g339755; PIDN:AAA36754.1; PID:g339756  
A;Accession: C36555  
A;Molecule type: protein  
A;Residues: 30-38;41-53, 'X', 55-79, 'XX', 82-94, 'NK', 'XX', 100-104;107-128;162-167,'X',169-2  
A;Note: the purified protein, called tumor necrosis factor binding protein, is a soluble  
R;Gray, P.W.; Barrett, K.; Chantry, D.; Turner, M.; Feldmann, M.  
Proc. Natl. Acad. Sci. U.S.A. 87, 7380-7384, 1990  
A;Title: Cloning of human tumor necrosis factor (TNF) receptor cDNA and expression of re  
A;Reference number: A38281; MUID:91017509; PMID:2170974  
A;Accession: A38281  
A;Molecule type: mRNA



A;Residues: 1-455 <GRA>  
A;Cross-references: GB:M37764  
A;Note: the authors translated the codon TGG for residue 371 as Thr, AAG for residue 372  
R;Nopnar, Y.; Kemper, O.; Brakebusch, C.; Engelmann, H.; Zhang, R.; Aderka, D.; Holtmann  
EMBO J. 9, 3269-3278, 1990  
A;Title: Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA for the type  
le form of the receptor.  
A;Reference number: S12057; MUID:91006021; PMID:1698610  
A;Accession: S12057  
A;Molecule type: mRNA  
A;Residues: 1-455 <NOP>  
A;Cross-references: EMBL:X55313; NID:G37223; PIDN:CAA39021.1; PID:G37224  
A;Note: parts of soluble TNF binding protein 1, including its amino and carboxyl ends, \*  
R;Kemper, O.; Wallach, D.  
Gene 134, 209-216, 1993  
A;Title: Cloning and partial characterization of the promoter for the human p55 tumor ne  
A;Reference number: JT0758; MUID:94085779; PMID:8262379  
A;Accession: JT0758  
A;Molecule type: DNA  
A;Residues: 1-13 <KEM>  
R;Seckinger, P.; Vey, E.; Turcatti, G.; Wingfield, P.; Dayer, J.M.  
Eur. J. Immunol. 20, 1167-1174, 1990  
A;Title: Tumor necrosis factor inhibitor: purification, NH-2-terminal amino acid sequenc  
A;Reference number: A60231; MUID:90292116; PMID:2113477  
A;Accession: A60231  
A;Molecule type: protein  
A;Residues: 41-43, 'X', 45-53, 'X', 55-57 <SEC>  
R;Gatanaga, T.; Hwang, C.; Kohr, W.; Cappuccini, F.; Lucci III, J.A.; Jeffes, E.W.B.; Le  
Proc. Natl. Acad. Sci. U.S.A. 87, 8781-8784, 1990  
A;Title: Purification and characterization of an inhibitor (soluble tumor necrosis facto  
tients.  
A;Reference number: A38258; MUID:91062364; PMID:2174164  
A;Accession: A38258  
A;Molecule type: protein  
A;Residues: 41-60 <GAT>  
A;Experimental source: cancer patient serum  
R;Olsson, I.; Lantz, M.; Nilsson, E.; Peetre, C.; Thysell, H.; Grubb, A.; Adolf, G.  
Eur. J. Haematol. 42, 270-275, 1989  
A;Title: Isolation and characterization of a tumor necrosis factor binding protein from  
A;Reference number: A60594; MUID:89171156; PMID:2924890  
A;Accession: A60594  
A;Molecule type: protein  
A;Residues: 41-43, 'X', 45-53, 'V', 55-57, 'XK', 60 <OLS>  
A;Experimental source: renal failure patient urine  
R;Engelmann, H.; Novick, D.; Wallach, D.  
J. Biol. Chem. 265, 1531-1536, 1990  
A;Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence  
A;Reference number: A35010; MUID:90110215; PMID:2153136  
A;Accession: A35010  
A;Molecule type: protein  
A;Residues: 41-45 <ENG>  
A;Experimental source: normal urine  
R;Kajihara, J.; Asada, A.; Kirihara, S.; Kato, K.  
Biosci. Biotechnol. Biochem. 58, 2266-2268, 1994  
A;Title: Amino acid sequence of natural tumor necrosis factor alpha inhibitor purified f  
A;Reference number: JC2404; MUID:95128033; PMID:7765720  
A;Accession: JC2404  
A;Molecule type: protein  
A;Residues: 41-53, 'X', 55-144, 'X', 146-150, 'X', 152-186, 'X', 188-201 <KAJ>  
A;Experimental source: urine  
C;Comment: This protein is one of two known receptors for both TNF-alpha (cachectin) and  
C;Genetics:  
A;Gene: GDB:TNFR1  
A;Cross-references: GDB:125913; OMIM:191190  
A;Map position: 12p13.2-12p13.2  
A;Introns: 13/3; 65/1; 108/1; 158/1; 184/2; 209/1; 247/1; 256/3; 353/1  
C;Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology  
C;Keywords: duplication; glycoprotein; receptor; transmembrane protein  
F;1-21/Domain: signal sequence #status predicted <SIG>  
F;22-455/Product: tumor necrosis factor receptor 1 #status predicted <MAT>  
F;30-211/Domain: extracellular #status predicted <EXT>  
F;41-201/Product: TNF binding protein 1 (tumor necrosis factor alpha inhibitor) #status  
F;44-82/Domain: NGF receptor repeat homology <NG1>

F;84-126/Domain: NGF receptor repeat homology <NG2>  
F;127-167/Domain: NGF receptor repeat homology <NG3>  
F;168-196/Domain: NGF receptor repeat homology <NG4>  
F;212-234/Domain: transmembrane #status predicted <MEM>  
F;235-455/Domain: intracellular #status predicted <INT>  
F;54,145,151/Binding site: carbohydrate (Asn) (covalent) #status predicted  
Query Match 100.0%; Score 582; DB 1; Length 455;  
Best Local Similarity 100.0%; Pred. No. 1.3e-52;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AHKPSLDTDDPATLYAVVENVPLRWKEFVRRRLGLSDHEIDRLQLNGRCLEAQYSML 60  
Db 345 AHKPSLDTDDPATLYAVVENVPLRWKEFVRRRLGLSDHEIDRLQLNGRCLEAQYSML 404  
QY 61 ATWRRTPREATLELLGRVLRMDLLGCLDIEEALCGPAALPPAPSLLR 111  
Db 405 ATWRRTPREATLELLGRVLRMDLLGCLDIEEALCGPAALPPAPSLLR 455  
RESULT 2  
JC4302  
tumor necrosis factor receptor p55 precursor - pig  
C;Species: Sus scrofa domestica (domestic pig)  
C;Date: 29-Nov-1995 #sequence\_revision 08-Feb-1996 #text\_change 23-Jul-1999  
C;Accession: JC4302; PC4093  
R;Suter, B.; Pauli, U.  
Gene 163, 263-266, 1995  
A;Title: Cloning of the cDNA encoding the porcine p55 tumor necrosis factor receptor.  
A;Reference number: JC4302; MUID:96011645; PMID:7590278  
A;Accession: JC4302  
A;Molecule type: mRNA  
A;Residues: 1-461 <SUT>  
A;Cross-references: GB:U19994; NID:g1141752; PIDN:AAC48499.1; PID:g1141753  
A;Accession: PC4093  
A;Molecule type: protein  
A;Residues: 1-7 <SU2>  
A;Experimental source: kidney cell line 15  
C;Genetics:  
A;Gene: tnfr  
C;Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology  
C;Keywords: glycoprotein; kidney; receptor; transmembrane protein; tumor  
F;1-29/Domain: signal sequence #status predicted <SIG>  
F;30-461/Product: tumor necrosis factor receptor p55 #status predicted <MAT>  
F;44-194/Domain: extracellular cysteine rich #status predicted <EXT>  
F;44-82/Domain: NGF receptor repeat homology <NG1>  
F;84-126/Domain: NGF receptor repeat homology <NGF>  
F;211-231/Domain: transmembrane #status predicted <TMM>  
F;361-447/Domain: signal transduction #status predicted <SIT>  
F;54,145,151/Binding site: carbohydrate (Asn) (covalent) #status predicted  
Query Match 79.5%; Score 462.5; DB 2; Length 461;  
Best Local Similarity 83.0%; Pred. No. 3.4e-40;  
Matches 93; Conservative 3; Mismatches 15; Indels 1; Gaps 1;  
QY 1 AHK-PQSLDTPATLYAVVENVPLRWKEFVRRRLGLSDHEIDRLQLNGRCLEAQYSM 59  
Db 350 AHSAPQLADADPATLYAVVDGVPPTRWKEFVRRRLGLSEIERLELQNGRCLEAQYSM 409  
QY 60 LATWRRTPREATLELLGRVLRMDLLGCLDIEEALCGPAALPPAPSLLR 111  
Db 410 LAEWRRTSRREATLELLGSVLRMDLLGCLDIEEALRGPARLAPAPHLR 461  
RESULT 3  
GQRTT1  
tumor necrosis factor receptor 1 precursor - rat  
N;Contains: tumor necrosis factor binding protein 1 (TNF blocking factor)  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 30-Jun-1992 #sequence\_revision 07-Oct-1994 #text\_change 22-Jun-1999  
C;Accession: B36555  
R;Himmler, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.; Pfizenmaier, K.; Lantz, M.;  
DNA Cell Biol. 9, 705-715, 1990













F;172-204/Domain: ankyrin repeat homology <AN05>  
F;205-237/Domain: ankyrin repeat homology <AN06>  
F;238-270/Domain: ankyrin repeat homology <AN07>  
F;271-303/Domain: ankyrin repeat homology <AN08>  
F;304-336/Domain: ankyrin repeat homology <AN09>  
F;337-369/Domain: ankyrin repeat homology <AN10>  
F;370-402/Domain: ankyrin repeat homology <AN11>  
F;403-435/Domain: ankyrin repeat homology <AN12>  
F;436-468/Domain: ankyrin repeat homology <AN13>  
F;469-501/Domain: ankyrin repeat homology <AN14>  
F;502-534/Domain: ankyrin repeat homology <AN15>  
F;535-567/Domain: ankyrin repeat homology <AN16>  
F;568-600/Domain: ankyrin repeat homology <AN17>  
F;601-633/Domain: ankyrin repeat homology <AN18>  
F;634-666/Domain: ankyrin repeat homology <AN19>  
F;667-699/Domain: ankyrin repeat homology <AN20>  
F;700-732/Domain: ankyrin repeat homology <AN21>  
F;733-765/Domain: ankyrin repeat homology <AN22>  
F;766-798/Domain: ankyrin repeat homology <AN23>

Query Match 13.7%; Score 80; DB 2; Length 1856;  
Best Local Similarity 30.1%; Pred. No. 8.4;  
Matches 25; Conservative 14; Mismatches 42; Indels 2; Gaps 2;

Qy 4 PQSLDTDDPATL-YAVVENVPPLRWKEFVRLGLSDHEIDRLQLNGRCCLREAQYSMLAT 62  
Db 1394 PGSLSGTEQAEMKMVAISEHGLGLSWAELARELQFSVEDINRIRVENPNSLLEQSVALLNL 1453

Qy 63 WRRRTPRREATLELLGRVLRDMD 85  
Db 1454 WVIR-EGQNANMENLYTALQSID 1475

Search completed: June 1, 2004, 14:47:08  
Job time : 11.6317 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 1, 2004, 14:33:56 ; Search time 7.97605 Seconds  
(without alignments)  
724.643 Million cell updates/sec

Title: US-09-854-906-8  
Perfect score: 582  
Sequence: 1 AHKPQSLDTPDPTLYAVVE.....DIEEALCGPAALPPAPSLLR 111

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues 141681  
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	582	100.0	455	1 TRIA_HUMAN	P19438 homo sapien
2	462.5	79.5	461	1 TRIA_PIG	P50555 sus scrofa
3	424	72.9	471	1 TRIA_BOVIN	O19131 bos taurus
4	386	66.3	461	1 TRIA_RAT	P22934 rattus norv
5	350.5	60.2	454	1 TRIA_MOUSE	P25118 mus musculu
6	167.5	28.8	417	1 TR25_HUMAN	Q93038 h tumor nec
7	100	17.2	381	1 T10B_MOUSE	Q9qzm4 mus musculu
8	91.5	15.7	671	1 RIK1_HUMAN	Q13546 homo sapien
9	90	15.5	656	1 RIK1_MOUSE	Q60855 mus musculu
10	86	14.8	1862	1 ANK1_MOUSE	Q02357 mus musculu
11	80.5	13.8	4377	1 ANK3_HUMAN	Q12955 homo sapien
12	80	13.7	1880	1 ANK1_HUMAN	P16157 homo sapien
13	77.5	13.3	591	1 STI1_SCHPO	Q9usi5 schizosacch
14	76.5	13.1	440	1 T10B_HUMAN	O14763 homo sapien
15	74.5	12.8	208	1 FADD_HUMAN	Q13158 homo sapien
16	74.5	12.8	3924	1 ANK2_HUMAN	Q01484 homo sapien
17	73	12.5	1199	1 Y173_HUMAN	Q14679 homo sapien
18	72.5	12.5	295	1 YJIE_LACLA	Q9cgy1 lactococcus
19	72.5	12.5	580	1 SYQ_XYLFA	Q9pdp1 xyliella fas
20	70.5	12.1	580	1 SYQ_XYLFT	Q87du6 xyliella fas
21	69.5	11.9	429	1 MURÄ_BRUME	Q8yff61 brucella me
22	69.5	11.9	1805	1 NEST_RAT	P21263 rattus norv
23	69.5	11.9	2390	1 SPCP_HUMAN	O15020 homo sapien
24	69	11.9	481	1 TPH_XENLA	Q92142 xenopus lae
25	69	11.9	1882	1 POL2_TRSVR	P25247 tomato ring
26	68.5	11.8	205	1 FADD_MOUSE	Q61160 mus musculu
27	68.5	11.8	354	1 HOM1_HUMAN	Q86ym7 homo sapien
28	68.5	11.8	1092	1 RHG7_MOUSE	Q9r0z9 mus musculu
29	68	11.7	445	1 TPH1_CHICK	P70080 gallus gall
30	68	11.7	521	1 ICEA_HUMAN	Q92851 homo sapien
31	68	11.7	554	1 PYRG_CORGL	Q8nql7 corynebacte
32	67.5	11.6	371	1 HEMZ_FALSO	Q8xw32 ralstonia s
33	67.5	11.6	468	1 T10A_HUMAN	O00220 homo sapien

34	67.5	11.6	1091	1 RHG7_RAT	Q63744 r rho-gtpas
35	66.5	11.4	189	1 YI35_PASMU	Q9ck03 pasteurella
36	66.5	11.4	323	1 LIPA_AGRTS	Q8ufg1 agrobacteri
37	66.5	11.4	332	1 TNR6_PIG	O77736 sus scrofa
38	66.5	11.4	781	1 NANH_VIBCH	P37060 vibrio chol
39	66.5	11.4	1091	1 RHG7_HUMAN	Q96qbl homo sapien
40	66.5	11.4	2388	1 SPCP_RAT	Q9qwn8 rattus norv
41	66	11.3	887	1 PMC2_MOUSE	P56960 mus musculu
42	66	11.3	1618	1 NEST_HUMAN	P48681 homo sapien
43	65.5	11.3	335	1 TNR6_HUMAN	P25445 homo sapien
44	65.5	11.3	366	1 HOM1_MOUSE	Q9z2y3 mus musculu
45	65.5	11.3	724	1 PRTP_PRVIF	P11871 pseudorabie

ALIGNMENTS

RESULT 1					
TR1A_HUMAN					
ID	TR1A_HUMAN	STANDARD;	PRT;	455 AA.	
AC	P19438;				
DT	01-FEB-1991 (Rel. 17, Created)				
DT	01-FEB-1991 (Rel. 17, Last sequence update)				
DT	15-MAR-2004 (Rel. 43, Last annotation update)				
DE	Tumor necrosis factor receptor superfamily member 1A precursor (p60)				
DE	(TNF-R1) (TNF-RI) (p55) (CD120a) [Contains: Tumor necrosis factor binding protein 1 (TBPI)].				
DE	TNFRSF1A OR TNFR1 OR TNFR.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Placenta;				
RX	MEDLINE=90235285; PubMed=2158863;				
RA	Schall T.J., Lewis M., Koller K.J., Lee A., Rice G.C., Wong G.H.W.,				
RA	Getanaga T., Granger G.A., Lentz R., Raab H., Kohr W.J., Goeddel D.V.;				
RT	"Molecular cloning and expression of a receptor for human tumor necrosis factor.";				
RL	Cell 61:361-370(1990).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=90235284; PubMed=2158862;				
RA	Loetscher H., Pan Y.-C.E., Lahm H.-W., Gentz R., Brockhaus M.,				
RA	Tabuchi H., Lesslauer W.;				
RT	"Molecular cloning and expression of the human 55 kd tumor necrosis factor receptor.";				
RL	Cell 61:351-359(1990).				
RN	[3]				
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 41-53; 110-124 AND 199-201.				
RX	MEDLINE=91006021; PubMed=1698610;				
RA	Nophar Y., Kemper O., Brakebusch C., Engelmann H., Zwang R.,				
RA	Aderka D., Holtmann H., Wallach D.;				
RT	"Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA for the type I TNF-R, cloned using amino acid sequence data of its soluble form, encodes both the cell surface and a soluble form of the receptor.";				
RL	EMBO J. 9:3269-3278(1990).				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=91090841; PubMed=1702293;				
RA	Himmler A., Maurer-Fogy I., Kroenke M., Scheurich P., Pfizenmaier K.,				
RA	Lantz M., Olsson I., Hauptmann R., Stratowa C., Adolf G.R.;				
RT	"Molecular cloning and expression of human and rat tumor necrosis factor receptor chain (p60) and its soluble derivative, tumor necrosis factor-binding protein.";				
RL	DNA Cell Biol. 9:705-715(1990).				
RN	[5]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Placenta;				
RX	MEDLINE=91017509; PubMed=2170974;				
RA	Gray P.W., Barrett K., Chantry D., Turner M., Feldman M.;				

RT "Cloning of human tumor necrosis factor (TNF) receptor cDNA and  
RT expression of recombinant soluble TNF-binding protein.";  
RL Proc. Natl. Acad. Sci. U.S.A. 87:7380-7384(1990).  
RN [6]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92250049; PubMed=1315717;  
RA Fuchs P., Strehl S., Dworzak M., Himmler A., Ambros P.F.;  
RA "Structure of the human TNF receptor 1 (p60) gene (TNFR1) and  
RT localization to chromosome 12p13.";  
RL Genomics 13:219-224(1992).  
RN [7]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length  
RT human and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [9]  
RP SEQUENCE OF 41-45.  
RX MEDLINE=90110215; PubMed=2153136;  
RA Engelmann H., Novick D., Wallach D.;  
RA "Two tumor necrosis factor-binding proteins purified from human  
RT urine. Evidence for immunological cross-reactivity with cell surface  
RT tumor necrosis factor receptors.";  
RL J. Biol. Chem. 265:1531-1536(1990).  
RN [10]  
RP INTERACTION WITH BAG4.  
RX MEDLINE=99115917; PubMed=9915703;  
RA Jiang Y., Woronicz J.D., Liu W., Goeddel D.V.;  
RA "Prevention of constitutive TNF receptor 1 signaling by silencer of  
RT death domains.";  
RL Science 283:543-546(1999).  
RN [11]  
RP X-RAY CRYSTALLOGRAPHY (2.85 ANGSTROMS) OF 30-211 IN COMPLEX WITH TNFB.  
RX MEDLINE=93258809; PubMed=8387891;  
RA Banner D.W., D'Arcy A., Janes W., Gentz R., Schoenfeld H.-J.,  
RA Broger C., Loetscher H., Lesslauer W.;  
RT "Crystal structure of the soluble human 55 kd TNF receptor-human TNF  
RT beta complex: implications for TNF receptor activation.";  
RL Cell 73:431-445(1993).  
RN [12]  
RP X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS) OF 41-202.  
RX MEDLINE=97094982; PubMed=8939750;  
RA Naismith J.H., Devine T.Q., Khono H., Sprang S.R.;  
RT "Structures of the extracellular domain of the type I tumor necrosis  
RT factor receptor.";  
RL Structure 4:1251-1262(1996).  
RN [13]  
RP VARIANTS FHF ARG-59; TYR-62; MET-79; PHE-81; ARG-117 AND TYR-117.  
RX MEDLINE=99213501; PubMed=10199409;  
RA McDermott M.F., Aksentijevich I., Galon J., McDermott E.M.,  
OGunkolade B.W., Centola M., Mansfield E., Gadina M., Karenko L.,  
Petersson T., McCarthy J., Frucht D.M., Aringer M., Torosyan Y.,  
Teppo A.-M., Wilson M., Karaarslan H.M., Wan Y., Todd I., Wood G.,  
Schlimgen R., Kumarajeewa T.R., Cooper S.M., Vella J.P., Amos C.I.,  
Mulley J., Quane K.A., Molloy M.G., Rnaki A., Powell R.J.,  
Hitman G.A., O'Shea J., Kastner D.L.;  
RT "Germline mutations in the extracellular domains of the 55 kDa TNF  
RT receptor, TNFR1, define a family of dominantly inherited  
RL autoinflammatory syndromes.";  
CC Cell 97:133-144(1999).  
CC -!- FUNCTION: Receptor for TNFSF2/TNF-alpha and homotrimeric  
CC TNFSF1/lymphotoxin-alpha. The adaptor molecule FADD recruits  
CC caspase-8 to the activated receptor. The resulting death-inducing  
CC signaling complex (DISC) performs caspase-8 proteolytic activation  
CC which initiates the subsequent cascade of caspases (aspartate-  
CC specific cysteine proteases) mediating apoptosis. Contributes to  
CC the induction of noncytotoxic TNF effects including anti-viral  
CC state and activation of the acid sphingomyelinase.  
CC -!- SUBUNIT: Binding of TNF to the extracellular domain leads to  
CC homotrimerization. The aggregated death domains provide a novel  
CC molecular interface that interacts specifically with the death  
CC domain of TRADD. Various TRADD-interacting proteins such as TRAFs,  
CC RIP and possibly FADD, are recruited to the complex by their  
CC association with TRADD. This complex activates at least two  
CC distinct signaling cascades, apoptosis and NF-kappa-B signaling.  
CC Binds BAG4.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein and secreted.  
CC -!- DOMAIN: The domain that induces A-SMASE is probably identical to  
CC the death domain. The N-SMASE activation domain (NSD) is both  
CC necessary and sufficient for activation of N-SMASE.  
CC -!- PTM: The soluble form is produced from the membrane form by  
CC proteolytic processing.  
CC -!- DISEASE: Defects in TNFRSF1A are a cause of autosomal dominant  
CC familial hibernian fever (FHF) [MIM:142680]. FHF is a disease  
CC characterized by recurrent fever, abdominal pain, localized tender  
CC skin lesions and myalgia.  
CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.  
CC -!- SIMILARITY: Contains 1 death domain.  
CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD120a entry;  
CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd120a.htm".  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL; X55313; CAA39021.1; -.  
CC EMBL; M33294; AAA03210.1; -.  
CC EMBL; M58286; AAA36753.1; -.  
CC EMBL; M63121; AAA36754.1; -.  
CC EMBL; M75866; AAA61201.1; -.  
CC EMBL; M75864; AAA61201.1; JOINED.  
CC EMBL; M75865; AAA61201.1; JOINED.  
CC EMBL; M60275; AAA36756.1; -.  
CC EMBL; A21522; CAA01558.1; -.  
CC EMBL; A131997; AAM77802.1; -.  
CC EMBL; BC010140; AAH10140.1; -.  
CC PIR; A38208; GQHUT1.  
CC PDB; 1TNR; 31-JUL-94.  
CC PDB; 1NCF; 07-DEC-95.  
CC PDB; 1EXT; 11-JAN-97.  
CC PDB; 1FT4; 12-OCT-01.  
CC PDB; 1ICH; 01-APR-02.  
CC Genew; HGNC:11916; TNFRSF1A.  
CC MIM; 191190; -.  
CC MIM; 142680; -.  
CC GO; GO:0005576; C:extracellular; TAS.  
CC GO; GO:0005887; C:integral to plasma membrane; TAS.  
CC GO; GO:0005032; F:tumor necrosis factor receptor cell differe...; TAS.  
CC GO; GO:0007165; P:signal transduction; TAS.



Query Match 100.0%; Score 582; DB 1; Length 455;  
Best Local Similarity 100.0%; Pred. No. 9e-54;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKPSLDTDDPATLYAVVENVPPLRWKEFVRRGLSDHEIDRLQLNGRCLREAQYSML 60  
Db 345 AHKPSLDTDDPATLYAVVENVPPLRWKEFVRRGLSDHEIDRLQLNGRCLREAQYSML 404

QY 61 ATWRRRTPRREATLELLGRVLRDMDLLGCLDIEEALCGPAALPPAPSLLR 111  
Db 405 ATWRRRTPRREATLELLGRVLRDMDLLGCLDIEEALCGPAALPPAPSLLR 455

RESULT 2  
TR1A\_PIG STANDARD; PRT; 461 AA.

AC P5055;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Tumor necrosis factor receptor superfamily member 1A precursor (p60)  
DE (TNF-R1) (TNF-RI) (p55).  
GN TNFRSF1A OR TNFR1.  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_TaxID=9823;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Kidney;  
RX MEDLINE=96011645; PubMed=7590278;  
RA Suter B., Pauli U.H.;  
RT "Cloning of the cDNA encoding the porcine p55 tumor necrosis factor receptor.";  
RL Gene 163:263-266(1995).

CC -!- FUNCTION: Receptor for TNFSF2/TNF-alpha and homotrimeric  
CC TNFSF1/lymphotoxin-alpha. The adaptor molecule FADD recruits  
CC caspase-8 to the activated receptor. The resulting death-inducing  
CC signaling complex (DISC) performs caspase-8 proteolytic activation  
CC which initiates the subsequent cascade of caspases (aspartate-  
CC specific cysteine proteases) mediating apoptosis (By similarity).  
CC -!- SUBUNIT: Binding of TNF to the extracellular domain leads to  
CC homotrimerization. The aggregated death domains provide a novel  
CC molecular interface that interacts specifically with the death  
CC domain of TRADD. Various TRADD-interacting proteins such as TRAFs,  
CC RIP and possibly FADD, are recruited to the complex by their  
CC association with TRADD. This complex activates at least two  
CC distinct signaling cascades, apoptosis and NF-kappa-B signaling.  
CC Binds BAG4 (By similarity).  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.  
CC -!- SIMILARITY: Contains 1 death domain.

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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC -----  
CC EMBL; U19994; AAC48499.1; -.  
CC PIR; JC4302; JC4302.  
CC HSSP; P19438; 1TNR.  
CC InterPro; IPR000488; Death.  
CC InterPro; IPR001368; TNFR\_c6.  
CC Pfam; PF00531; death; 1.  
CC Pfam; PF00020; TNFR\_c6; 3.  
CC SMART; SM00005; DEATH; 1.  
CC SMART; SM00208; TNFR; 4.  
CC PROSITE; PS00652; TNFR\_NGFR\_1; 3.  
CC PROSITE; PS50050; TNFR\_NGFR\_2; 2.

DR PROSITE; PS50017; DEATH\_DOMAIN; 1.  
KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.  
FT SIGNAL 1 21 POTENTIAL.  
FT CHAIN 22 461 TUMOR NECROSIS FACTOR RECEPTOR  
FT SUPERFAMILY MEMBER 1A.  
FT DOMAIN 22 210 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 211 233 POTENTIAL.  
FT DOMAIN 234 461 CYTOPLASMIC (POTENTIAL).  
FT REPEAT 43 82 TNFR-CYS 1.  
FT REPEAT 83 125 TNFR-CYS 2.  
FT REPEAT 126 166 TNFR-CYS 3.  
FT REPEAT 167 195 TNFR-CYS 4.  
FT DOMAIN 340 350 N-SMASE ACTIVATION DOMAIN (NSD).  
FT DOMAIN 362 447 DEATH.  
FT DISULFID 44 58 BY SIMILARITY.  
FT DISULFID 59 72 BY SIMILARITY.  
FT DISULFID 62 81 BY SIMILARITY.  
FT DISULFID 84 99 BY SIMILARITY.  
FT DISULFID 102 117 BY SIMILARITY.  
FT DISULFID 105 125 BY SIMILARITY.  
FT DISULFID 127 143 BY SIMILARITY.  
FT DISULFID 146 158 BY SIMILARITY.  
FT DISULFID 149 166 BY SIMILARITY.  
FT DISULFID 168 179 BY SIMILARITY.  
FT DISULFID 182 194 BY SIMILARITY.  
FT DISULFID 185 190 BY SIMILARITY.  
FT CARBOHYD 54 54 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 86 86 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 145 145 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 151 151 N-LINKED (GLCNAC. .) (POTENTIAL).  
SQ SEQUENCE 461 AA; 50696 MW; CD72361EC60C9D43 CRC64;

Query Match 79.5%; Score 462.5; DB 1; Length 461;  
Best Local Similarity 83.0%; Pred. No. 3.5e-41;  
Matches 93; Conservative 3; Mismatches 15; Indels 1; Gaps 1;

QY 1 AHK-PQSLDTDDPATLYAVVENVPPLRWKEFVRRGLSDHEIDRLQLNGRCLREAQYSM 59  
Db 350 AHSAPAQLADADPATLYAVVDGVPPTRWKEFVRRGLSEHEIERLELQNGRCLREAQYSM 409

QY 60 LATWRRRTPRREATLELLGRVLRDMDLLGCLDIEEALCGPAALPPAPSLLR 111  
Db 410 LAEWRRTSRREATLELLGSLVRDMDLLGCLDIEEALGPARLAPAPHLLR 461

RESULT 3  
TR1A\_BOVIN STANDARD; PRT; 471 AA.

AC O19131;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Tumor necrosis factor receptor superfamily member 1A precursor (p60)  
DE (TNF-R1) (TNF-RI) (p55).  
GN TNFRSF1A OR TNFR1.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Aorta;  
RX MEDLINE=98273505; PubMed=9613449;  
RA Lee E.-K., Kehrl M.E. Jr., Taylor M.J.;  
RT "Cloning and sequencing of cDNA encoding bovine tumor necrosis factor (TNF)-receptor I.";  
RL Vet. Immunol. Immunopathol. 61:379-385(1998).  
CC -!- FUNCTION: Receptor for TNFSF2/TNF-alpha and homotrimeric  
CC TNFSF1/lymphotoxin-alpha. The adaptor molecule FADD recruits  
CC caspase-8 to the activated receptor. The resulting death-inducing  
CC signaling complex (DISC) performs caspase-8 proteolytic activation  
CC which initiates the subsequent cascade of caspases (aspartate-

```
CC specific cysteine proteases) mediating apoptosis (By similarity).
CC -!- SUBUNIT: Binding of TNF to the extracellular domain leads to
CC homotrimerization. The aggregated death domains provide a novel
CC molecular interface that interacts specifically with the death
CC domain of TRADD. Various TRADD-interacting proteins such as TRAFs,
CC RIP and possibly FADD, are recruited to the complex by their
CC association with TRADD. This complex activates at least two
CC distinct signaling cascades, apoptosis and NF-kappa-B signaling.
CC Binds BAG4 (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC -!- SIMILARITY: Contains 1 death domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U90937; AAB65143.1; -.
CC HSSP; P19438; 1TNR.
CC InterPro; IPR000488; Death.
CC InterPro; IPR001368; TNFR_c6.
CC Pfam; PF00531; death; 1.
CC SMART; SM00005; DEATH; 1.
CC SMART; SM00208; TNFR; 3.
CC PROSITE; PS00652; TNFR_NGFR_1; 3.
CC PROSITE; PS50050; TNFR_NGFR_2; 3.
CC PROSITE; PS50017; DEATH_DOMAIN; 1.
CC Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
KW SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 471 TUMOR NECROSIS FACTOR RECEPTOR
FT DOMAIN 22 210 SUPERFAMILY MEMBER 1A.
FT TRANSMEM 211 233 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 234 471 POTENTIAL.
FT REPEAT 43 82 CYTOPLASMIC (POTENTIAL).
FT REPEAT 83 125 TNFR-CYS 1.
FT REPEAT 126 166 TNFR-CYS 2.
FT REPEAT 167 195 TNFR-CYS 3.
FT DOMAIN 340 360 TNFR-CYS 4.
FT DOMAIN 372 457 N-SMASE ACTIVATION DOMAIN (NSD).
FT DISULFID 44 58 DEATH.
FT DISULFID 59 72 BY SIMILARITY.
FT DISULFID 62 81 BY SIMILARITY.
FT DISULFID 84 99 BY SIMILARITY.
FT DISULFID 102 117 BY SIMILARITY.
FT DISULFID 105 125 BY SIMILARITY.
FT DISULFID 127 143 BY SIMILARITY.
FT DISULFID 146 158 BY SIMILARITY.
FT DISULFID 149 166 BY SIMILARITY.
FT DISULFID 168 179 BY SIMILARITY.
FT DISULFID 182 194 BY SIMILARITY.
FT DISULFID 185 190 BY SIMILARITY.
FT CARBOHYD 54 54 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 145 145 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 151 151 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 471 AA; 51367 MW; 5243EF514DF81C4 CRC64;

Query Match 72.9%; Score 424; DB 1; Length 471;
Best Local Similarity 79.4%; Pred. No. 4.1e-37;
Matches 85; Conservative 5; Mismatches 17; Indels 0; Gaps 0;

QY 4 PQSLDTPATLYAVVNPPLRWKEFVRRRLGLSDHEIDRLQLNGRCLREAQYSMLATW 63
Db 364 PDQLADADPATLYAVVDGVPSPRWKELVRRRLGLSEHEIERLENGRHLREAQYSMLAAW 423

QY 64 RRRTPRREATLELLGRVLRDMDLLGCLIEDIEEALCGPAALPPAPSLL 110
Db 424 RRRTPRREATLELLGRVLRDMDLLGCLENIEEALGGAARLASEPRLL 470
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RESULT 4
TR1A_RAT
ID TR1A_RAT STANDARD; PRT; 461 AA.
AC P22934; Q91V30; Q91Y93;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 1A precursor (p60)
DE (TNF-R1) (TNF-RI) (p55).
DE TNFRSF1A OR TNFR1 OR TNFR-1.
GN Rattus norvegicus (Rat).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91090841; PubMed=1702293;
RA Himmler A., Maurer-Fogy I., Kroenke M., Scheurich P., Pfizenmaier K.,
RA Lantz M., Olsson I., Hauptmann R., Stratowa C., Adolf G.R.;
RT "Molecular cloning and expression of human and rat tumor necrosis
RT factor receptor chain (p60) and its soluble derivative, tumor
RT necrosis factor-binding protein.";
RL DNA Cell Biol. 9:705-715(1990).
RN [2]
RP SEQUENCE FROM N.A., AND VARIANTS VAL-230 AND PRO-295.
RC STRAIN=BB(DR)/Wor, LEW/NHsd, ACI/SegHsd, DA/Bkl, F344/NHsd, and
RC BN/SSNHsd;
RA Furuya T., Salstrom J.L., Bina J., Hashimoto A., Dobbins D.E.,
RA Wilder R.L., Remmers E.F.;
RT "Polymorphisms of the tumor necrosis factor receptor type 1 locus
RT among autoimmune susceptible and resistant inbred rat strains.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Receptor for TNFSF2/TNF-alpha and homotrimeric
CC TNFSF1/lymphotoxin-alpha. The adaptor molecule FADD recruits
CC caspase-8 to the activated receptor. The resulting death-inducing
CC signaling complex (DISC) performs caspase-8 proteolytic activation
CC which initiates the subsequent cascade of caspases (aspartate-
CC specific cysteine proteases) mediating apoptosis (By similarity).
CC -!- SUBUNIT: Binding of TNF to the extracellular domain leads to
CC homotrimerization. The aggregated death domains provide a novel
CC molecular interface that interacts specifically with the death
CC domain of TRADD. Various TRADD-interacting proteins such as TRAFs,
CC RIP and possibly FADD, are recruited to the complex by their
CC association with TRADD. This complex activates at least two
CC distinct signaling cascades, apoptosis and NF-kappa-B signaling.
CC Binds BAG4 (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC -!- SIMILARITY: Contains 1 death domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M63122; AAA42256.1; -.
CC EMBL; AF329976; AAK53562.1; -.
CC EMBL; AF329977; AAK53563.1; -.
CC EMBL; AF329981; AAK53567.1; -.
CC EMBL; AF329978; AAK53564.1; -.
CC EMBL; AF329979; AAK53565.1; -.
CC EMBL; AF329980; AAK53566.1; -.
CC PIR; B36555; GQRTT1.
CC HSSP; P19438; INCF.
CC InterPro; IPR000488; Death.
CC InterPro; IPR001368; TNFR_c6.
CC Pfam; PF00531; death; 1.
CC Pfam; PF00020; TNFR_c6; 4.
```

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DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 3.
DR PROSITE; PS50050; TNFR_NGFR_2; 3.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 461 TUMOR NECROSIS FACTOR RECEPTOR
FT SUPERFAMILY MEMBER 1A.
FT DOMAIN 22 211 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 212 234 POTENTIAL.
FT DOMAIN 235 461 CYTOPLASMIC (POTENTIAL).
FT REPEAT 43 82 TNFR-CYS 1.
FT REPEAT 83 125 TNFR-CYS 2.
FT REPEAT 126 166 TNFR-CYS 3.
FT REPEAT 167 196 TNFR-CYS 4.
FT DOMAIN 344 354 N-SMASE ACTIVATION DOMAIN (NSD).
FT DOMAIN 363 448 DEATH.
FT DISULFID 44 58 BY SIMILARITY.
FT DISULFID 59 72 BY SIMILARITY.
FT DISULFID 62 81 BY SIMILARITY.
FT DISULFID 84 99 BY SIMILARITY.
FT DISULFID 102 117 BY SIMILARITY.
FT DISULFID 105 125 BY SIMILARITY.
FT DISULFID 127 143 BY SIMILARITY.
FT DISULFID 146 158 BY SIMILARITY.
FT DISULFID 149 166 BY SIMILARITY.
FT DISULFID 168 179 BY SIMILARITY.
FT DISULFID 182 195 BY SIMILARITY.
FT DISULFID 185 191 BY SIMILARITY.
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 201 201 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 230 230 I -> V (IN STRAINS LEW/NHSD, ACI/SEGHSD,
FT DA/BKL AND F344/NHSD).
FT VARIANT 295 295 H -> P (IN STRAINS LEW/NHSD, ACI/SEGHSD,
FT DA/BKL, F344/NHSD AND BN/SSNHSD).
SQ SEQUENCE 461 AA; 50969 MW; EB23C05450FBD202 CRC64;

Query Match 66.3%; Score 386; DB 1; Length 461;
Best Local Similarity 73.3%; Pred. No. 4e-33;
Matches 74; Conservative 10; Mismatches 17; Indels 0; Gaps 0;

QY 1 AHKQSLDTPATLYAVVENVPLRWKEFVRRRLGLSDHEIDRLQLONGRCLEAQYSL 60
Db 352 AAQPQLDTADPAMLYAVVDGVPPTRWKEFMRLGLSEHEIERLELQNGRCLEAHYSML 411

QY 61 ATWRRTPRREATLELLGRVLRLMDLGLCLEDIEEALCGPA 101
Db 412 EAWRRTPRHEATLDVGRVLCMDNLRGCLNIRETLESPA 452

RESULT 5
TR1A MOUSE
ID TR1A MOUSE STANDARD; PRT; 454 AA.
AC P25118;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 1A precursor (p60)
DE (TNF-R1) (TNF-R1) (p55).
GN TNFRSF1A OR TNFR1 OR TNFR-1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91187885; PubMed=1849278;
RA Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C.,
RA Wong G.H., Chen E.Y., Goeddel D.V.;
RT "Cloning and expression of cDNAs for two distinct murine tumor
RT necrosis factor receptors demonstrate one receptor is species
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RT specific.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91246168; PubMed=1645445;
RA Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I.,
RA Copeland N.G., Jenkins N.A., Smith C.A.;
RT "Molecular cloning and expression of the type 1 and type 2 murine
RT receptors for tumor necrosis factor.";
RL Mol. Cell. Biol. 11:3020-3026(1991).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=91285014; PubMed=1647956;
RA Barrett K., Taylor-Fishwick D.A., Cope A.P., Kissonerghis A.M.,
RA Gray P.W., Feldmann M., Foxwell B.M.J.;
RT "Cloning, expression and cross-linking analysis of the murine p55
RT tumor necrosis factor receptor.";
RL Eur. J. Immunol. 21:1649-1656(1991).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=92039815; PubMed=1657766;
RA Rothe J.G., Brockhaus M., Gentz R., Lesslauer W.;
RT "Molecular cloning and expression of the mouse Tnf receptor type b.";
RL Immunogenetics 34:338-340(1991).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=94245292; PubMed=8188324;
RA Bebo B.F., Linthicum D.S.;
RT "Nucleotide sequence of the TNF type I receptor from a mouse
RT endothelioma cell line.";
RL Immunogenetics 39:450-451(1994).
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE=93156721; PubMed=8381516;
RA Rothe J., Bluethmann H., Gentz R., Lesslauer W., Steinmetz M.;
RT "Genomic organization and promoter function of the murine tumor
RT necrosis factor receptor beta gene.";
RL Mol. Immunol. 30:165-175(1993).
RN [7]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/He; TISSUE=Mesenchyme;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.S., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Receptor for TNFSF2/TNF-alpha and homotrimeric
CC TNFSF1/lymphotoxin-alpha. The adaptor molecule FADD recruits
CC caspase-8 to the activated receptor. The resulting death-inducing
CC signaling complex (DISC) performs caspase-8 proteolytic activation
CC which initiates the subsequent cascade of caspases (aspartate-
CC specific cysteine proteases) mediating apoptosis (By similarity).
CC -!- SUBUNIT: Binding of TNF to the extracellular domain leads to
CC homotrimerization. The aggregated death domains provide a novel
CC molecular interface that interacts specifically with the death
CC domain of TRADD. Various TRADD-interacting proteins such as TRAFs,
```



CC RIP and possibly FADD, are recruited to the complex by their  
CC association with TRADD. This complex activates at least two  
CC distinct signaling cascades, apoptosis and NF-kappa-B signaling.  
CC Binds BAG4 (By similarity).  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.  
CC -!- SIMILARITY: Contains 1 death domain.  
CC -----  
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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CC use by non-profit institutions as long as its content is in no way  
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL; M60468; AAA39751.1; -.  
CC EMBL; M59377; AAA40464.1; -.  
CC EMBL; X59238; CAA41922.1; -.  
CC EMBL; X57796; CAA40936.1; -.  
CC EMBL; L26349; AAA59361.1; -.  
CC EMBL; M76656; AAA40465.1; -.  
CC EMBL; M88067; AAA40465.1; JOINED.  
CC EMBL; M76655; AAA40465.1; JOINED.  
CC EMBL; BC004599; AAH04599.1; -.  
CC EMBL; BC052675; AAH52675.1; -.  
CC PIR; A38634; GQMST1.  
CC HSSP; P19438; 1EXT.  
CC MGD; MGI:1314884; Tnfrsfla.  
CC GO; GO:0007166; P:cell surface receptor linked signal transdu. . .; IMP.  
CC GO; GO:0006952; P:defense response; IMP.  
CC GO; GO:0006954; P:inflammatory response; IMP.  
CC GO; GO:0007515; P:lymph gland development; IMP.  
CC InterPro; IPR000488; Death.  
CC InterPro; IPR001368; TNFR\_c6.  
CC Pfam; PF00531; death; 1.  
CC Pfam; PF00020; TNFR\_c6; 4.  
CC SMART; SM00005; DEATH; 1.  
CC SMART; SM00208; TNFR; 4.  
CC PROSITE; PS00652; TNFR\_NGFR\_1; 3.  
CC PROSITE; PS50050; TNFR\_NGFR\_2; 3.  
CC PROSITE; PS50017; DEATH\_DOMAIN; 1.  
KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.  
FT SIGNAL 1 21 POTENTIAL.  
FT CHAIN 22 454 TUMOR NECROSIS FACTOR RECEPTOR  
FT SUPERFAMILY MEMBER 1A.  
FT DOMAIN 22 212 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 213 235 POTENTIAL.  
FT DOMAIN 236 454 CYTOPLASMIC (POTENTIAL).  
FT REPEAT 43 82 TNFR-CYS 1.  
FT REPEAT 83 125 TNFR-CYS 2.  
FT REPEAT 126 166 TNFR-CYS 3.  
FT REPEAT 167 196 TNFR-CYS 4.  
FT DOMAIN 339 349 N-SMASE ACTIVATION DOMAIN (NSD).  
FT DOMAIN 356 441 DEATH.  
FT DISULFID 44 58 BY SIMILARITY.  
FT DISULFID 59 72 BY SIMILARITY.  
FT DISULFID 62 81 BY SIMILARITY.  
FT DISULFID 84 99 BY SIMILARITY.  
FT DISULFID 102 117 BY SIMILARITY.  
FT DISULFID 105 125 BY SIMILARITY.  
FT DISULFID 127 143 BY SIMILARITY.  
FT DISULFID 146 158 BY SIMILARITY.  
FT DISULFID 149 166 BY SIMILARITY.  
FT DISULFID 168 179 BY SIMILARITY.  
FT DISULFID 182 195 BY SIMILARITY.  
FT DISULFID 185 191 BY SIMILARITY.  
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 202 202 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CONFLICT 394 394 R -> G (IN REF. 6).  
SQ SEQUENCE 454 AA; 50129 MW; 0710C2E8C3C2B6D9 CRC64;

Query Match 60.2%; Score 350.5; DB 1; Length 454;  
Best Local Similarity 69.3%; Pred. No. 2.2e-29;  
Matches 70; Conservative 10; Mismatches 20; Indels 1; Gaps 1;  
  
QY 1 AHKPSLDTDTPATLYAVVENVPPLRWKEFVRLGLSDHEIDRLLELQNGRCLREAQYSML 60  
Db 346 AH-PQRPDNADLAILYAVVDGPPPARWKEFMFGLSEHEIERLEMQNGRCLREAQYSML 404  
  
QY 61 ATWRRRTPRREATLELGRVLRMDMLLGCLDEIEEALCGPA 101  
Db 405 EAWRRRTPRHEDTLEVGVLVSKMNLGCLNILEALRNPA 445  
  
RESULT 6  
TR25\_HUMAN  
ID TR25\_HUMAN STANDARD; PRT; 417 AA.  
AC Q93038; Q00275; Q00276; Q00277; Q00278; Q00279; Q00280; Q14865;  
AC Q14866; P78507; P78515; Q92983; Q93036; Q93037; Q99722; Q99830;  
AC Q99831; Q9BY86; Q9UME0; Q9UME1; Q9UME5;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Tumor necrosis factor receptor superfamily member 25 precursor  
DE (WSL-1 protein) (Apoptosis-mediating receptor DR3) (Apoptosis-  
DE mediating receptor TRAMP) (Death domain receptor 3) (WSL protein)  
DE (Apoptosis inducing receptor AIR) (Apo-3) (Lymphocyte associated  
DE receptor of death) (LARD).  
GN TNFRSF25 OR TNFRSF12 OR WSL1 OR WSL OR APO3 OR DR3 OR DDR3.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORMS 1; 3 AND 4), AND MUTAGENESIS.  
RC TISSUE=Lymphoid;  
RX MEDLINE=97088617; PubMed=8934525;  
RA Kitson J., Raven T., Jiang Y.-P., Goeddel D.V., Giles K.M., Pun K.-T.,  
RA Grinham C.J., Brown R., Farrow S.N.;  
RA "A death-domain-containing receptor that mediates apoptosis.";  
RL Nature 384:372-375(1996).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RC TISSUE=Umbilical vein endothelial cells;  
RX MEDLINE=97081063; PubMed=8875942;  
RA Chinnaiyan A.M., O'Rourke K., Yu G.-L., Lyons R.H., Garg M.,  
RA Duan D.R., Xing L., Gentz R., Ni J., Dixit V.M.;  
RT "Signal transduction by DR3, a death domain-containing receptor  
RT related to TNFR-1 and CD95.";  
RL Science 274:990-992(1996).  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Degli-Esposti M.A., Din W.S., Cosman D., Smith C.A., Goodwin R.G.;  
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RC TISSUE=Heart;  
RX MEDLINE=97148200; PubMed=8994832;  
RA Marsters S.A., Sheridan J.P., Donahue C.J., Pitti R.M., Gray C.L.,  
RA Goddard A.D., Bauer K.D., Ashkenazi A.;  
RT "Apo-3, a new member of the tumor necrosis factor receptor family,  
RT contains a death domain and activates apoptosis and NF-kappa-B.";  
RL Curr. Biol. 6:1669-1676(1996).  
RN [5]  
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3; 4; 5; 6; 7; 8; 9 AND 10).  
RX MEDLINE=97272273; PubMed=9114039;  
RA Screaton G.R., Xu X.-N., Olsen A.L., Cowper A.E., Tan R.,  
RA McMichael A.J., Bell J.I.;  
RT "LARD: a new lymphoid-specific death domain containing receptor  
RT regulated by alternative pre-mRNA splicing.";  
RL Proc. Natl. Acad. Sci. U.S.A. 94:4615-4619(1997).  
RN [6]  
RP SEQUENCE FROM N.A. (ISOFORMS 11 AND 12).  
RX MEDLINE=98113360; PubMed=9446802;















DE Ankyrin 1 (Erythrocyte ankyrin).

GN ANK1 OR ANK-1.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Erythrocyte;

RX MEDLINE=92345717; PubMed=1386265;

RA White R.A., Birkenmeier C.S., Peters L.L., Barker J.E., Lux S.E.;

RT "Murine erythrocyte ankyrin cDNA: highly conserved regions of the regulatory domain.";

RL Mamm. Genome 3:281-285(1992).

CC -!- FUNCTION: Attach integral membrane proteins to cytoskeletal elements; bind to the erythrocyte membrane protein band 4.2, to Na-K ATPase, to the lymphocyte membrane protein GP85, and to the cytoskeletal proteins fodrin, tubulin, vimentin and desmin.

CC Erythrocyte ankyrins also link spectrin (beta chain) to the cytoplasmic domain of the erythrocytes anion exchange protein; they retain most or all of these binding functions.

CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC SURFACE OF ERYTHROCYTIC PLASMA MEMBRANE.

CC -!- PTM: Regulated by phosphorylation (By similarity).

CC -!- PTM: Acylated by palmitic acid group(s) (By similarity).

CC -!- SIMILARITY: Contains 23 ANK repeats.

CC -!- SIMILARITY: Contains 1 death domain.

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DR EMBL; M84756; AAA37236.1; --.

DR PIR; I49502; I49502.

DR HSSP; Q00420; IAWC.

DR MGD; MGI:88024; Ank1.

DR InterPro; IPR002110; ANK.

DR InterPro; IPR000488; Death.

DR InterPro; IPR000906; ZU5.

DR Pfam; PF00023; ank; 24.

DR Pfam; PF00531; death; 1.

DR Pfam; PF00791; ZU5; 1.

DR PRINTS; PR01415; ANKYRIN.

DR SMART; SM00248; ANK; 22.

DR SMART; SM00005; DEATH; 1.

DR SMART; SM00218; ZU5; 1.

DR PROSITE; PS50088; ANK\_REPEAT; 20.

DR PROSITE; PS50297; ANK\_REPEAT\_REGION; 1.

DR PROSITE; PS50017; DEATH\_DOMAIN; 1.

KW Cytoskeleton; Repeat; ANK repeat; 89 kDa DOMAIN (ANION EXCHANGE PROTEIN DOMAIN 1 827

FT DOMAIN 1 827

FT BINDING DOMAIN).

FT 62 kDa DOMAIN (SPECTRIN BINDING DOMAIN).

FT 55 kDa REGULATORY DOMAIN (REGULATES THE BINDING OF ANKYRIN TO SPECTRIN AND THE BAND 3 PROTEIN).

FT ANK 1.

FT ANK 2.

FT ANK 3.

FT ANK 4.

FT ANK 5.

FT ANK 6.

FT ANK 7.

FT ANK 8.

FT ANK 9.

FT ANK 10.

FT ANK 11.

FT ANK 12.

FT REPEAT 40 69

FT REPEAT 73 102

FT REPEAT 106 135

FT REPEAT 139 168

FT REPEAT 170 197

FT REPEAT 201 230

FT REPEAT 234 263

FT REPEAT 267 296

FT REPEAT 300 329

FT REPEAT 333 362

FT REPEAT 366 395

FT REPEAT 399 428

FT REPEAT 432 461 ANK 13.

FT REPEAT 465 494 ANK 14.

FT REPEAT 498 527 ANK 15.

FT REPEAT 531 560 ANK 16.

FT REPEAT 564 593 ANK 17.

FT REPEAT 597 626 ANK 18.

FT REPEAT 630 659 ANK 19.

FT REPEAT 663 692 ANK 20.

FT REPEAT 696 725 ANK 21.

FT REPEAT 729 758 ANK 22.

FT REPEAT 762 791 ANK 23.

FT DOMAIN 1399 1483 DEATH.

SQ SEQUENCE 1862 AA; 204242 MW; AE6B85B5B29001E5 CRC64;

Query Match 14.8%; Score 86; DB 1; Length 1862;

Best Local Similarity 23.4%; Pred. No. 0.78;

Matches 32; Conservative 19; Mismatches 48; Indels 38; Gaps 4;

Qy 8 DTDDPATLYAVVENVPPLRWKVFVRRRLGLSDHEIDRLQLONGRCCLREAQYSMLATWRRRT 67

Db 1395 DTRVEMRMMAVIREHLGLSWAELARELQFSVEDINRIRVENPNSLLDQSTALLTLWVDR- 1453

Qy 68 PRREATLELLGRVLRDMD---LLGCL------DI 93

Db 1454 EGENAKMENLYTALRNIDRSEIVNMLEGSRQSRNLKPERRHGDRREYSLSPSQVNGYSSL 1513

Qy 94 EBALCGPAALP---PAP 107

Db 1514 QDELLSPASLQYALPSP 1530

RESULT 11

ANK3\_HUMAN

ID ANK3\_HUMAN STANDARD; PRT; 4377 AA.

AC Q12955;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Ankyrin 3 (ANK-3) (Ankyrin G).

GN ANK3.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain stem;

RX MEDLINE=95138209; PubMed=7836469;

RA Kordeli E., Lambert S., Bennett V.;

RT "AnkyrinG. A new ankyrin gene with neural-specific isoforms localized at the axonal initial segment and node of Ranvier.";

RL J. Biol. Chem. 270:2352-2359(1995).

CC -!- FUNCTION: Membrane-cytoskeleton linker. The neural-specific isoforms may participate in the maintenance/targeting of ion channels and cell adhesion molecules at the nodes of Ranvier and axonal initial segments.

CC -!- SUBUNIT: Neural-specific isoforms may be a constituent of a neurofascin/NRCAM/ankyrin G complex.

CC -!- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=1;

CC Comment=A number of isoforms are produced;

CC Name=1; Synonyms=480-kDa isoform;

CC IsoId=Q12955-1; Sequence=Displayed;

CC -!- TISSUE SPECIFICITY: Expressed in brain and other tissues. Isoform 1 is neural-specific.

CC -!- SIMILARITY: Contains 23 ANK repeats.

CC -!- SIMILARITY: Contains 1 death domain.

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CC -----

DR EMBL; D85197; BAA22619.1; --  
DR EMBL; AL049498; CAB39910.1; --  
DR PIR; T41531; T41531.  
DR PIR; T51996; T51996.  
DR HSSP; P53041; 1A17.  
DR GeneDB SPombe; SPOC645.14c; --  
DR InterPro; IPR006636; STI1.  
DR InterPro; IPR008941; TPR-like.  
DR InterPro; IPR001440; TPR.  
DR Pfam; PF00515; TPR; 8.  
DR SMART; SM00727; STI1; 2.  
DR SMART; SM00028; TPR; 8.  
KW Heat shock; TPR repeat; Repeat.  
FT REPEAT 2 35 TPR 1.  
FT REPEAT 37 69 TPR 2.  
FT REPEAT 70 103 TPR 3.  
FT REPEAT 265 298 TPR 4.  
FT REPEAT 299 331 TPR 5.  
FT REPEAT 339 372 TPR 6.  
FT REPEAT 399 432 TPR 7.  
FT REPEAT 434 466 TPR 8.  
FT REPEAT 467 500 TPR 9.  
FT CONFLICT 28 28 A -> T (IN REF. 1).  
SQ SEQUENCE 591 AA; 65544 MW; D218FCCD5884B4AA CRC64;

Query Match 13.3%; Score 77.5; DB 1; Length 591;  
Best Local Similarity 32.4%; Pred. No. 1.7;  
Matches 24; Conservative 14; Mismatches 25; Indels 11; Gaps 3;  
QY 40 EIDRLQLQGRCLREAQ-----YSMLATWRRRTTPREATLELLGRVLRDMDLLGCLLED- 92  
Db 495 EVDREPTGKLNREIESQLSKCMSASQR---QNETEEETMARIQKDPVILQDP 550  
QY 93 IEEALCGPAALPPA 106  
Db 551 AMQAILQARENPA 564

RESULT 14  
T10B\_HUMAN STANDARD; PRT: 440 AA.  
AC O14763; O14720; O15508; O15517; O15531; Q9BVE0;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Tumor necrosis factor receptor superfamily member 10B precursor (Death  
DE receptor-2) (TRAIL-R2).  
DE TNFRSF10B OR DR5 OR TRAILR2 OR TRICK2 OR KILLER OR ZTNFR9.  
GN Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM LONG), AND SEQUENCE OF N-TERMINUS.  
RC TISSUE=Foreskin fibroblast;  
RX MEDLINE=97459925; PubMed=9311998;  
RA Walczak H., Degli-Esposti M.A., Johnson R.S., Smolak P.J., Waugh J.Y.,  
RA Boiani N., Timour M.S., Gerhart M.J., Schooley K.A., Smith C.A.,  
RA Goodwin R.G., Rauch C.T.;  
RT "TRAIL-R2: a novel apoptosis-mediating receptor for TRAIL.";  
RL EMBO J. 16:5386-5397(1997).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT), ALTERNATIVE  
RP SPLICING, AND VARIANTS LEU-32 AND VAL-67.  
RX MEDLINE=97431692; PubMed=9285725;  
RA Screaton G.R., Mongkolsapaya J., Xu X.-N., Cowper A.E.,  
RA McMichael A.J., Bell J.I.;

RT "TRICK2, a new alternatively spliced receptor that transduces the  
RT cytotoxic signal from TRAIL.";  
RL Curr. Biol. 7:693-696(1997).  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORM LONG), CHARACTERIZATION, AND VARIANTS  
RP LEU-32 AND VAL-67.  
RC TISSUE=Liver, and Spleen;  
RX MEDLINE=98039016; PubMed=9373179;  
RA Schneider P., Bodmer J.-L., Thome M., Hofmann K., Holler N.,  
RA Tschopp J.;  
RT "Characterization of two receptors for TRAIL.";  
RL FEBS Lett. 416:329-334(1997).  
RN [4]  
RP SEQUENCE FROM N.A. (ISOFORM SHORT).  
RC TISSUE=Ovary;  
RX MEDLINE=97467719; PubMed=9326928;  
RA Wu G.S., Burns T.F., McDonald E.R. III, Jiang W., Meng R.,  
RA Krantz I.D., Kao G., Gan D.D., Zhou J.Y., Muschel R., Hamilton S.R.,  
RA Spinner N.B., Markowitz S., Wu G., el-Deiry W.S.;  
RT "KILLER/DR5 is a DNA damage-inducible p53-regulated death receptor  
RT gene.";  
RL Nat. Genet. 17:141-143(1997).  
RN [5]  
RP SEQUENCE FROM N.A. (ISOFORM SHORT).  
RX MEDLINE=97390508; PubMed=9242610;  
RA Pan G., Ni J., Wei Y.-F., Yu G.-I., Gentz R., Dixit V.M.;  
RT "An antagonist decoy receptor and a death domain-containing receptor  
RT for TRAIL.";  
RL Science 277:815-818(1997).  
RN [6]  
RP SEQUENCE FROM N.A. (ISOFORM SHORT), AND VARIANTS LEU-32 AND VAL-67.  
RX MEDLINE=97467318; PubMed=9325248;  
RA MacFarlane M., Ahmad M., Srinivasula S.M., Fernandes-Alnemri T.,  
RA Cohen G.M., Alnemri E.S.;  
RT "Identification and molecular cloning of two novel receptors for the  
RT cytotoxic ligand TRAIL.";  
RL J. Biol. Chem. 272:25417-25420(1997).  
RN [7]  
RP SEQUENCE FROM N.A. (ISOFORM SHORT), AND VARIANTS LEU-32 AND VAL-67.  
RX MEDLINE=98090092; PubMed=9430227;  
RA Chaudhary P.M., Eby M., Jasmin A., Bookwalter A., Murray J., Hood L.;  
RT "Death receptor 5, a new member of the TNFR family, and DR4 induce  
RT FADD-dependent apoptosis and activate the NF-kappaB pathway.";  
RL Immunity 7:821-830(1997).  
RN [8]  
RP SEQUENCE FROM N.A. (ISOFORM SHORT), AND VARIANT LEU-32.  
RX MEDLINE=97390509; PubMed=9242611;  
RA Sheridan J.P., Marsters S.A., Pitti R.M., Gurney A., Skubatch M.,  
RA Baldwin D., Ramakrishnan L., Gray C.L., Baker K., Wood W.I.,  
RA Goddard A.D., Godowski P., Ashkenazi A.;  
RT "Control of TRAIL-induced apoptosis by a family of signaling and decoy  
RT receptors.";  
RL Science 277:818-821(1997).  
RN [9]  
RP SEQUENCE FROM N.A. (ISOFORM LONG), AND VARIANTS LEU-32 AND VAL-67.  
RA Arai T., Akiyama Y., Okabe S., Saito K., Iwai T., Yuasa Y.;  
RT "Genomic structure and mutation analyses of the DR5/TRAIL receptor 2  
RT gene in colorectal carcinoma.";  
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.  
RN [10]  
RP SEQUENCE FROM N.A. (ISOFORM SHORT).  
RA Cao X., Zhang W., Wan T.;  
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
RN [11]  
RP SEQUENCE FROM N.A. (ISOFORM SHORT), AND VARIANTS LEU-32 AND VAL-67.  
RA Farrah T., Vu T., Gilbert T., Gross J., O'Hara P.;  
RT "Homo sapiens homolog of tumor necrosis factor receptor.";  
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
RN [12]  
RP SEQUENCE FROM N.A. (ISOFORM LONG), AND VARIANT LEU-32.  
RC TISSUE=Cervix;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,







GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 1, 2004, 14:35:21 ; Search time 33.2335 Seconds  
(without alignments)  
1053.831 Million cell updates/sec

Title: US-09-854-906-8  
Perfect score: 582  
Sequence: 1 AHKPQSLDTDDPATLYAVVE.....DIEEALCGPAALPPAPSLLR 111

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0  
Maximum DB seq length: 20000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL 25:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp Vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvirus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	477.5	82.0	446	6 Q95ND3	Q95nd3 felis silve
2	158	27.1	387	11 Q8VD70	Q8vd70 mus musculu
3	152	26.1	413	11 Q99MM1	Q99mm1 mus musculu
4	86	14.8	1848	11 Q61302	Q61302 mus musculu
5	83.5	14.3	368	13 Q57408	Q57408 meleagris g
6	83	14.3	273	5 Q9V8H5	Q9v8h5 drosophila
7	83	14.3	410	13 Q7T3M8	Q7t3m8 gallus gall
8	82.5	14.2	365	12 Q81645	Q81645 hepatitis c
9	82.5	14.2	3011	12 Q913D4	Q913d4 hepatitis c
10	82	14.1	163	17 Q9YBB1	Q9ybb1 aeropyrum p
11	81.5	14.0	364	12 Q68797	Q68797 hepatitis c
12	81.5	14.0	365	12 Q81652	Q81652 hepatitis c
13	81.5	14.0	3011	12 Q81754	Q81754 hepatitis c
14	81.5	14.0	3022	12 Q68798	Q68798 hepatitis c
15	81	13.9	626	16 Q9KXP5	Q9kyp5 streptomyce
16	80.5	13.8	143	11 Q70510	Q70510 rattus norv

17	80.5	13.8	314	6 Q861W6	Q861w6 felis silve
18	80.5	13.8	838	11 Q9QXH1	Q9qxh1 mus musculu
19	80.5	13.8	960	11 Q8VDA0	Q8vda0 rattus norv
20	80.5	13.8	1093	11 Q8CBN3	Q8cbn3 mus musculu
21	80.5	13.8	1726	11 Q8VC68	Q8vc68 mus musculu
22	80.5	13.8	1762	11 Q88521	Q88521 rattus norv
23	80.5	13.8	1887	4 Q7Z3G4	Q7z3g4 homo sapien
24	80.5	13.8	1943	11 Q61307	Q61307 mus musculu
25	80.5	13.8	2622	11 Q70511	Q70511 rattus norv
26	80	13.7	1038	11 Q80ZZ7	Q80zz7 mus musculu
27	80	13.7	1050	11 Q8CCV0	Q8ccv0 mus musculu
28	80	13.7	1719	4 Q13768	Q13768 homo sapien
29	80	13.7	1856	4 Q99407	Q99407 homo sapien
30	79	13.6	303	5 Q9NHG0	Q9nhg0 drosophila
31	79	13.6	965	4 Q7Z344	Q7z344 homo sapien
32	79	13.6	1863	4 Q7Z3L5	Q7z3l5 homo sapien
33	78.5	13.5	319	6 Q9TV79	Q9tv79 oryctolagus
34	78.5	13.5	320	6 Q9XS29	Q9xs29 oryctolagus
35	78.5	13.5	388	16 Q97PS5	Q97ps5 streptococc
36	78.5	13.5	634	5 Q8STZ1	Q8stz1 encephalito
37	78.5	13.5	811	4 Q9H0P5	Q9h0p5 homo sapien
38	77.5	13.3	356	10 Q8GRN3	Q8grn3 oryza sativ
39	77	13.2	202	13 Q9DEY7	Q9dey7 poephila gu
40	77	13.2	316	16 Q9HXZ2	Q9hxz2 pseudomonas
41	76.5	13.1	205	4 Q7Z2I8	Q7z2i8 homo sapien
42	76.5	13.1	364	12 Q68824	Q68824 hepatitis c
43	76.5	13.1	364	12 Q68805	Q68805 hepatitis c
44	76.5	13.1	634	5 Q8ST44	Q8st44 encephalito
45	75.5	13.0	364	12 Q92543	Q92543 hepatitis c

ALIGNMENTS

RESULT 1  
Q95ND3  
ID Q95ND3 PRELIMINARY; PRT; 446 AA.  
AC Q95ND3;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Tumor necrosis factor type I.  
GN TNFR I.  
OS Felis silvestris catus (Cat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
OX NCBI\_TaxID=9685;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Mizuno T., Goto Y., Baba K., Masuda K., Ohno K., Tsujimoto H.;  
RT "Molecular cloning of feline tumor necrosis factor receptor type I  
RT (TNFR I ) and expression of TNFR I and TNFR II in various disease in  
RT cats.";  
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB051103; BAB55455.1; -.  
DR GO; GO:0005489; F:electron transporter activity; IEA.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR GO; GO:0006118; P:electron transport; IEA.  
DR GO; GO:0007165; P:signal transduction; IEA.  
DR InterPro; IPR000345; CytC\_heme\_BS.  
DR InterPro; IPR000488; Death.  
DR InterPro; IPR006209; EGF like.  
DR InterPro; IPR01368; TNFR\_c6.  
DR Pfam; PF00531; death; 1.  
DR Pfam; PF00020; TNFR\_c6; 4.  
DR SMART; SM00005; DEATH; 1.  
DR SMART; SM00208; TNFR; 4.  
DR PROSITE; PS00190; CYTOCHROME C; 1.  
DR PROSITE; PS0017; DEATH\_DOMAIN; 1.  
DR PROSITE; PS01186; EGF 2; 1.  
DR PROSITE; PS00652; TNFR\_NGFR 1; 3.  
DR PROSITE; PS00050; TNFR\_NGFR 2; 3.  
SQ SEQUENCE 446 AA; 49563 MW; 217BD331DD8A74AA CRC64;





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DR InterPro; IPR000906; ZU5.
DR Pfam; PF00023; ank; 24.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00791; ZU5; 1.
DR PRINTS; PR01415; ANKYRIN.
DR SMART; SM00248; ANK; 22.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00218; ZU5; 1.
DR PROSITE; PS50088; ANK_REPEAT; 20.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
KW ANK repeat; Repeat.
SQ SEQUENCE 1848 AA; 202577 MW; 5744BECBF9EBA056 CRC64;

Query Match 14.8%; Score 86; DB 11; Length 1848;
Best Local Similarity 23.4%; Pred. No. 4.9;
Matches 32; Conservative 19; Mismatches 48; Indels 38; Gaps 4;

QY 8 DTDDPATLYAVVENVPLRWKEFVRLRLGLSDHEIDRLRLQNGRCLREAQYSMLATWRRRT 67
Db 1411 DTDRVEMRMVIREHGLGSLWAELARELQFSVEDINRIRVENPNSLDDQSTALLTLWDR- 1469

QY 68 PRREATLELLGRVLRDMD---LLGCLL-----DI 93
Db 1470 EGENAKMENLYTALNRIDRSEIVNMLEVSGQRNLKPERRHGDREYSLSPSQVNGYSSL 1529

QY 94 EEALCGPAALP---PAP 107
Db 1530 QDELLSPASLOALPSP 1546

RESULT 5
O57408
ID O57408 PRELIMINARY; PRT; 368 AA.
AC O57408;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Subgroup E ALV receptor.
OS Meleagris gallopavo (Common turkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Meleagris.
OX NCBI_TaxID=9103;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97471016; PubMed=9326659;
RA Adkins H.B., Brojatsch J., Naughton J., Rolls M.M., Pesola J.M.,
RA Young J.A.;
RT "Identification of a cellular receptor for subgroup E avian leukosis
RT virus.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:11617-11622 (1997).
DR EMBL; AF006002; AAB93987.1; -.
DR HSSP; O14763; IDOG.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0005840; C:ribosome; IEA.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR001450; 4Fe4S ferredoxin.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001865; Ribosomal_S2.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00198; 4FE4S_FERREDOXIN; 1.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR PROSITE; PS00962; RIBOSOMAL_S2_1; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
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DR PROSITE; PS50050; TNFR_NGFR_2; 2.
KW Receptor.
SQ SEQUENCE 368 AA; 41020 MW; 5701AC2A6D4F87E2 CRC64;

Query Match 14.3%; Score 83.5; DB 13; Length 368;
Best Local Similarity 30.4%; Pred. No. 1.5;
Matches 28; Conservative 15; Mismatches 42; Indels 7; Gaps 3;

QY 11 DPATLYA-----VVENVPPLRWKEFVRLRLGLSDHEIDRLRLQNGRCLREAQYSMLATWRR 65
Db 268 DPITVLSSEFTFVDLVFPFQWRFRGRALGRNNLYQAE-QNDRESGEPLYQMLIMWLN 326

QY 66 RTPREATLELLGRVLRDMDLLGCLLEIEAL 97
Db 327 KEGSK-ASVNTLLETLSQISLSGVADIASEL 357

RESULT 6
Q9V8H5
ID Q9V8H5 PRELIMINARY; PRT; 273 AA.
AC Q9V8H5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE CG5576 protein (GH20785P).
GN IMD OR CG5576.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Berkeley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrera S., Fleischmann W.,
RA Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
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RN  [2]
RP  SEQUENCE FROM N.A.
RC  STRAIN=Berkeley;
RA  Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA  Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA  Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA  Nunoo J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
RA  Yu C., Lewis S.E., Rubin G.M., Celniker S.;
RL  Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AE003799; AAF57692.1; -.
DR  EMBL; AY051558; AAK92982.1; -.
DR  FlyBase; FBgn0013983; imd.
DR  GO; GO:0006961; P:antibacterial humoral response (sensu Inver. . .; IMP.
DR  GO; GO:0006963; P:antibacterial polypeptide induction; IMP.
DR  GO; GO:0006959; P:humoral immune response; IMP.
DR  InterPro; IPR000488; Death.
DR  Pfam; PF00531; death; 1.
DR  PROSITE; PS50017; DEATH DOMAIN; 1.
SQ  SEQUENCE 273 AA; 29899 MW; 7247CA4B46F5545B CRC64;

Query Match 14.3%; Score 83; DB 5; Length 273;
Best Local Similarity 24.8%; Pred. No. 1.2;
Matches 26; Conservative 25; Mismatches 38; Indels 16; Gaps 3;

QY 3 KPQSLDTPATLYAVVEN--VPPLR-----WKFEVRLGLSDHEIDR--LEL 46
Db 153 KPRASATRKTVSIVAMQSQEEDVRLDDVSTHLGEGWKQVMDLGMSEGQIDQALIDH 212
QY 47 QNGRCLEAQYSMLATWRRRTPRREATLELLGRVLRDMDLLGLCLE 91
Db 213 QMHGNIREVIYQLLQWIRSSADGVATVGRLTTLWESQHRDCVQ 257

RESULT 7
Q7T3M8
ID Q7T3M8 PRELIMINARY; PRT; 410 AA.
AC Q7T3M8;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Death domain-containing tumor necrosis factor receptor superfamily
DE member 23 variant 1 (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Bridgham J.T., Johnson A.L.;
RT "Identification and characterization of alternatively spliced, ovarian
RT enhanced death receptor and decoy receptor."
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY251408; AAP41833.1; -.
KW Receptor.
FT NON TER 410 410
SQ SEQUENCE 410 AA; 46194 MW; 4BFC7C7016C2BA60 CRC64;

Query Match 14.3%; Score 83; DB 13; Length 410;
Best Local Similarity 25.7%; Pred. No. 1.9;
Matches 18; Conservative 21; Mismatches 29; Indels 2; Gaps 2;

QY 16 YAVVENVPPLRWKEFVRLGLSDHEIDRLQLNGRCLEAQYSMLATWRRRTPRREATLE 75
Db 325 FAFIKEVPVKWRKLM-RTHLEENDIDKIIYNWPNIDIEQSYQMLLMWKNMGEKQSIK 383
QY 76 LLGRVLRDMD 85
Db 384 LLDE-LWDID 392

RESULT 8
Q81645
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ID Q81645 PRELIMINARY; PRT; 365 AA.
AC Q81645;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE NS5 (Genome polyprotein) (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YS117;
RX MEDLINE=94172337; PubMed=8126459;
RA Okamoto H., Kojima M., Sakamoto M., Iizuka H., Hadiwandowo S.,
RA Suwignyo S., Miyakawa Y., Mayumi M.;
RT "The entire nucleotide sequence and classification of a hepatitis C
RT virus isolate of a novel genotype from an Indonesian patient with
RT chronic liver disease."
RL J. Gen. Virol. 75:629-635(1994).
DR EMBL; D16190; BAA03731.1; -.
DR GO; GO:0019012; C:virion; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR GO; GO:0019079; P:viral genome replication; IEA.
DR InterPro; IPR002166; HCV_RdRP.
DR InterPro; IPR007094; RNA_pol_PsVir.
DR Pfam; PF00998; Viral_RdRP; 1.
KW Nonstructural protein; Polyprotein; RNA-directed RNA polymerase;
KW Transferase.
FT NON TER 1 1
SQ SEQUENCE 365 AA; 40296 MW; B5DAD6519868B630 CRC64;

Query Match 14.2%; Score 82.5; DB 12; Length 365;
Best Local Similarity 27.8%; Pred. No. 1.9;
Matches 35; Conservative 12; Mismatches 38; Indels 41; Gaps 6;

QY 2 HKPQSLDTPATLYAVVENVPPLRWKEFVRL--GL-----SDHEIDRLQLNGRCL 52
Db 212 HLEKALDCE---IYGAVHSVQPLDLPEIIQRLHGLSAFSLHSYSPGEINRV---AACL 263
QY 53 REAQYSMLATWRRRTPRREATLELLGRVLRDMDLLGLCLEIDEEALCG-----PAA 102
Db 264 RKLGVPPPLRAWHRARSVRATLLSQG-----KAAICGKYLEFNWAVTKLK 309
QY 103 LPPAPS 108
Db 310 LTPPLS 315

RESULT 9
Q913D4
ID Q913D4 PRELIMINARY; PRT; 3011 AA.
AC Q913D4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Genome polyprotein.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RA Guntaka R.V., Munnally S.K., Khaja M.N., Kota K.K., Ramana V.K.,
RA Swaminathan S., Sakata Y., Habeebullah C.M.;
RT "Nucleotide Sequence of Indian strain of Hepatitis C Virus."
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS;
```

CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF  
CC PROTEIN C AND MRNA (BY SIMILARITY).

DR EMBL; AY051292; AAK95832.1; --  
DR MEROPS; S29.001; --  
DR MEROPS; U39.001; --  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019028; C:viral capsid; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0008026; F:ATP dependent helicase activity; IEA.  
DR GO; GO:0005489; F:electron transporter activity; IEA.  
DR GO; GO:0003723; F:RNA binding; IEA.  
DR GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.  
DR GO; GO:0008236; F:serine-type peptidase activity; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR GO; GO:0016740; F:transferase activity; IEA.  
DR GO; GO:0006118; P:electron transport; IEA.  
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
DR GO; GO:0006350; P:transcription; IEA.  
DR GO; GO:0019079; P:viral genome replication; IEA.  
DR GO; GO:0019087; P:viral transformation; IEA.  
DR InterPro; IPR009003; Cys\_Ser\_trypsin.  
DR InterPro; IPR000345; CytC\_heme\_BS.  
DR InterPro; IPR001410; DEAD.  
DR InterPro; IPR002522; HCV\_capsid.  
DR InterPro; IPR002521; HCV\_core.  
DR InterPro; IPR002519; HCV\_env.  
DR InterPro; IPR002531; HCV\_NS1.  
DR InterPro; IPR002518; HCV\_NS2.  
DR InterPro; IPR000745; HCV\_NS4a.  
DR InterPro; IPR001490; HCV\_NS4b.  
DR InterPro; IPR002868; HCV\_NS5a.  
DR InterPro; IPR002166; HCV\_RdRP.  
DR InterPro; IPR004109; Peptidase\_C29.  
DR InterPro; IPR007095; RNA\_pol\_DS\_Ps.  
DR InterPro; IPR007094; RNA\_pol\_PSVir.  
DR Pfam; PF01543; HCV\_capsid; 1.  
DR Pfam; PF01542; HCV\_core; 1.  
DR Pfam; PF01539; HCV\_env; 1.  
DR Pfam; PF01560; HCV\_NS1; 1.  
DR Pfam; PF01538; HCV\_NS2; 1.  
DR Pfam; PF02907; HCV\_NS3; 1.  
DR Pfam; PF01006; HCV\_NS4a; 1.  
DR Pfam; PF01001; HCV\_NS4b; 1.  
DR Pfam; PF01506; HCV\_NS5a; 1.  
DR Pfam; PF00998; Viral\_RdRP; 1.  
DR ProDom; PD186062; HCV\_NS1; 1.  
DR SMART; SM00487; DEXDC; 1.  
DR PROSITE; PS00190; CYTOCHROME C; 1.

KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;  
KW Polyprotein; RNA-directed RNA polymerase; Transferase; Transmembrane.  
SQ SEQUENCE 3011 AA; 327234 MW; 57A21964B4227B60 CRC64;

Query Match 14.2%; Score 82.5; DB 12; Length 3011;  
Best Local Similarity 26.0%; Pred. No. 20;  
Matches 33; Conservative 13; Mismatches 40; Indels 41; Gaps 5;

QY 2 HKPQSLDTPATLYAVVENVPPLRWKEFVRRL-----GLSDHEIDRLQLNGRCL 52  
Db 2858 HLGKALDCE---IYGAVHSVQPLDLPEIIQRLHLSAFSLHSYSPGEINRV----AACL 2909

QY 53 REAQYSMLATWRRRTPREATLELLGRVLRMDLLGCLEDIEEALCG-----PAA 102  
Db 2910 RKLGVPPPLRAWRRHRSVRATLLSQG-----KAAICGKYLEFNWAVTKLK 2955

QY 103 LPPAPSL 109  
Db 2956 LTPLPSM 2962

RESULT 10  
Q9YBB1  
ID Q9YBB1 PRELIMINARY; PRT; 163 AA.

AC Q9YBB1;  
DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE 163AA long hypothetical methylmalonyl-CoA mutase alpha-subunit.  
GN APE1686.  
OS Aeropyrum pernix.  
OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcates;  
OC Desulfurococcaceae; Aeropyrum.  
OX NCBI\_TaxID=56636;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=K1;  
RX MEDLINE=99310339; PubMed=10382966;  
RA Kwarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,  
RA Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H.,  
RA Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,  
RA Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,  
RA Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K.,  
RA Nakamura Y., Nomura N., Sato Y., Kikuchi H.;  
RT "Complete genome sequence of an aerobic hyper-thermophilic  
crenarchaeon, Aeropyrum pernix K1.";  
RL DNA Res. 6:83-101(1999).  
DR EMBL; AP000062; BAA80687.1; --  
DR PIR; B72550; B72550.  
DR HSSP; P11653; 1REQ.  
DR GO; GO:0016853; F:isomerase activity; IEA.  
DR InterPro; IPR006159; Acid\_CoA\_mut\_C.  
DR InterPro; IPR006158; B12-binding.  
DR Pfam; PF02310; B12-binding; 1.  
DR TIGRFAMs; TIGR00640; acid\_CoA\_mut\_C; 1.  
KW Complete proteome.  
SQ SEQUENCE 163 AA; 17969 MW; C0BD5F04FBFED4A6 CRC64;

Query Match 14.1%; Score 82; DB 17; Length 163;  
Best Local Similarity 32.9%; Pred. No. 0.85;  
Matches 23; Conservative 13; Mismatches 28; Indels 6; Gaps 2;

QY 19 VENVPPLRWKEFVRRLGLSDHEIDRLQLNGRCLFEAQYSMLATWRRRTPREATLELLG 78  
Db 13 VLGTPTRRRYKVLVAKMGLDGH--DRGAKVVARALRDAGFEVVTGLRQTPEQVA---MA 66  
QY 79 RVLRDMDLLG 88  
Db 67 AVQEDVDVIG 76

RESULT 11  
Q68797  
ID Q68797 PRELIMINARY; PRT; 364 AA.  
AC Q68797;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE NS5 (Genome polyprotein) (Fragment).  
OS Hepatitis C virus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
OC Hepacivirus.  
OX NCBI\_TaxID=111103;  
RN [1] --  
RP SEQUENCE FROM N.A.  
RC STRAIN=JK046;  
RX MEDLINE=96226020; PubMed=8627233;  
RA Tokita H., Okamoto H., Iizuka H., Kishimoto J., Tsuda F.,  
RA Leimana L.A., Miyakawa Y., Mayumi M.;  
RT "Hepatitis C virus variants from Jakarta, Indonesia classifiable into  
novel genotypes in the second (2e and 2f), tenth (10a) and eleventh  
(11a) genetic groups.";  
RL J. Gen. Virol. 77:293-301(1996).  
DR EMBL; D49763; BAA08597.1; --  
DR GO; GO:0019012; C:virion; IEA.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0003723; F:RNA binding; IEA.





DR Pfam; PF01539; HCV env; 1.  
DR Pfam; PF01560; HCV\_NS1; 1.  
DR Pfam; PF01538; HCV\_NS2; 1.  
DR Pfam; PF02907; HCV\_NS3; 1.  
DR Pfam; PF01006; HCV\_NS4a; 1.  
DR Pfam; PF01001; HCV\_NS4b; 1.  
DR Pfam; PF01506; HCV\_NS5a; 1.  
DR Pfam; PF00998; Viral RdRP; 1.  
DR ProDom; PD186062; HCV\_NS1; 1.  
DR SMART; SM00487; DEXDc; 1.  
KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;  
KW Polyprotein; RNA-directed RNA polymerase; Transferase; Transmembrane.  
FT CHAIN 1 191  
FT CHAIN 192 383  
FT CHAIN 384 809  
FT CHAIN 810 1006  
FT CHAIN 1007 1657  
FT CHAIN 1658 1972  
FT CHAIN 1973 3011  
SQ SEQUENCE 3011 AA; 327212 MW; 9C16C120F4E79268 CRC64;  
  
Query Match 14.0%; Score 81.5; DB 12; Length 3011;  
Best Local Similarity 27.8%; Pred. No. 25;  
Matches 35; Conservative 11; Mismatches 39; Indels 41; Gaps 6;  
  
Qy 2 HKPQSLDTPDTPATLYAVVENVPLRWKEFVRRLL-GL-----SDHEIDRLQLNGRCL 52  
Db 2858 HLEKALDCE---IYGAVHSVQPLDPEIIQRLHGLSAFSLHSGYSPGEINRV---AACL 2909  
  
Qy 53 REAQYSLMATWRRTPRREATLELLGRVLRDMDLLGCLIEDIEEALCG-----PAA 102  
Db 2910 RKLGVPLRAWRHRARSVRATLLSQGG-----RAAICGKYLFWAVTKLK 2955  
  
Qy 103 LPPAPS 108  
Db 2956 LTPLPS 2961  
  
RESULT 14  
Q68798  
ID Q68798 PRELIMINARY; PRT; 3022 AA.  
AC Q68798;  
DT 01-NOV-1996 (TremBLrel. 01, Created)  
DT 01-NOV-1996 (TremBLrel. 01, Last sequence update)  
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)  
DE Genome polyprotein.  
OS Hepatitis C virus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
OC Hepacivirus.  
OX NCBI\_TaxID=11103;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=JK046;  
RX MEDLINE=96226020; PubMed=8627233;  
RA Tokita H., Okamoto H., Iizuka H., Kishimoto J., Tsuda F.,  
RA Lesmana L.A., Miyakawa Y., Mayumi M.;  
RT "Hepatitis C virus variants from Jakarta, Indonesia classifiable into  
RT novel genotypes in the second (2e and 2f), tenth (10a) and eleventh  
RT (11a) genetic groups."  
RL J. Gen. Virol. 77:293-301(1996).  
CC -1- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A  
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:  
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF  
CC PROTEIN C AND MRNA (BY SIMILARITY).  
DR EMBL; D63822; BAA09891.1; -.  
DR HSSP; P27958; 1HEI.  
DR MEROPS; S29.001; -.  
DR MEROPS; U39.001; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019028; C:viral capsid; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0008026; F:ATP dependent helicase activity; IEA.

DR GO; GO:0003723; F:RNA binding; IEA.  
DR GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.  
DR GO; GO:0008236; F:serine-type peptidase activity; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR GO; GO:0016740; F:transferase activity; IEA.  
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
DR GO; GO:0006350; P:transcription; IEA.  
DR GO; GO:0019079; P:viral genome replication; IEA.  
DR GO; GO:0019087; P:viral transformation; IEA.  
DR InterPro; IPR009003; Cys\_Ser\_trypsin.  
DR InterPro; IPR001410; DEAD.  
DR InterPro; IPR002522; HCV capsid.  
DR InterPro; IPR002521; HCV\_core.  
DR InterPro; IPR002519; HCV env.  
DR InterPro; IPR002531; HCV\_NS1.  
DR InterPro; IPR002518; HCV\_NS2.  
DR InterPro; IPR000745; HCV\_NS4a.  
DR InterPro; IPR001490; HCV\_NS4b.  
DR InterPro; IPR002868; HCV\_NS5a.  
DR InterPro; IPR002166; HCV RdRP.  
DR InterPro; IPR004109; Peptidase C29.  
DR InterPro; IPR007095; RNA\_pol\_DS\_PS.  
DR InterPro; IPR007094; RNA\_pol\_PSVir.  
DR Pfam; PF01543; HCV\_capsid; 1.  
DR Pfam; PF01542; HCV\_core; 1.  
DR Pfam; PF01539; HCV env; 1.  
DR Pfam; PF01560; HCV\_NS1; 1.  
DR Pfam; PF01538; HCV\_NS2; 1.  
DR Pfam; PF02907; HCV\_NS3; 1.  
DR Pfam; PF01006; HCV\_NS4a; 1.  
DR Pfam; PF01001; HCV\_NS4b; 1.  
DR Pfam; PF01506; HCV\_NS5a; 1.  
DR Pfam; PF00998; Viral RdRP; 1.  
DR ProDom; PD186062; HCV\_NS1; 1.  
DR SMART; SM00487; DEXDc; 1.  
KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;  
KW Polyprotein; RNA-directed RNA polymerase; Transferase; Transmembrane.  
SQ SEQUENCE 3022 AA; 328683 MW; EE6A21538FEA26E1 CRC64;  
  
Query Match 14.0%; Score 81.5; DB 12; Length 3022;  
Best Local Similarity 28.0%; Pred. No. 25;  
Matches 30; Conservative 12; Mismatches 32; Indels 33; Gaps 5;  
  
Qy 2 HKPQSLDTPDTPATLYAVVENVPLRWKEFVRRLL-----GLSDHEIDRLQLNGRCL 52  
Db 2871 HK--ALDFD---MYGVYNTITPLDLPLQIIQRLHGMMAFSLHGYSPGELNRV----GACL 2920  
  
Qy 53 REAQYSLMATWRRTPRREATLELLGRVLRDMDLLGCLIEDIEEALCG 99  
Db 2921 RKLGAAPLRAWRHRARAVRAKLIQGG-----KAAICG 2953  
  
RESULT 15  
Q9KYP5  
ID Q9KYP5 PRELIMINARY; PRT; 626 AA.  
AC Q9KYP5;  
DT 01-OCT-2000 (TremBLrel. 15, Created)  
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)  
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)  
DE Putative serine/threonine protein kinase.  
GN SCO4488 OR SCD69.08.  
OS Streptomyces coelicolor.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Streptomycineae; Streptomycetaceae; Streptomyces.  
OX NCBI\_TaxID=1902;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=A3(2);  
RA Oliver K., Harris D.;  
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=A3(2);



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 1, 2004, 14:30:06 ; Search time 48.521 Seconds  
(without alignments)  
646.376 Million cell updates/sec

Title: US-09-854-906-9  
Perfect score: 557  
Sequence: 1 ETVAINLSDDVLSKYITIA.....KIQTIILKDTSDSENSNFR 111

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*  
1: Geneseqp1980s:\*  
2: Geneseqp1990s:\*  
3: Geneseqp2000s:\*  
4: Geneseqp2001s:\*  
5: Geneseqp2002s:\*  
6: Geneseqp2003as:\*  
7: Geneseqp2003bs:\*  
8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	557	100.0	111	5	ABB81750	Abb81750 Tumour ne
2	557	100.0	121	5	ABB81752	Abb81752 Tumour ne
3	557	100.0	314	2	AAR76238	Aar76238 Fas-delta
4	557	100.0	314	2	AAR99682	Aar99682 Human Fas
5	557	100.0	314	2	AAW98070	Aaw98070 Soluble F
6	557	100.0	335	2	AAR28084	Aar28084 Human cel
7	557	100.0	335	2	AAR78606	Aar78606 Human Fas
8	557	100.0	335	2	AAR99681	Aar99681 Human Fas
9	557	100.0	335	2	AAR92528	Aar92528 hFas from
10	557	100.0	335	2	AAW50289	Aaw50289 Human Fas
11	557	100.0	335	2	AAW49104	Aaw49104 Fas prote
12	557	100.0	335	3	AAB01335	Aab01335 CD-95 (FA
13	557	100.0	335	3	AAB19341	Aab19341 Amino aci
14	557	100.0	335	3	AAB36267	Aab36267 Human Fas
15	557	100.0	335	4	AAB50517	Aab50517 Human tum
16	557	100.0	335	6	ABU07407	Abu07407 Protein d
17	557	100.0	335	6	ABR43905	Abr43905 Human GEN
18	557	100.0	436	3	AAW91026	Aay91026 Apoptobod
19	557	100.0	669	2	AAW64484	Aaw64484 Human TNF
20	550	98.7	431	4	AAW97650	Aay97650 CD44Hextr
21	550	98.7	431	6	ABU04641	Abu04641 Human exp
22	550	98.7	436	4	AAW97651	Aay97651 CD44Hextr
23	550	98.7	436	6	ABU04642	Abu04642 Human exp
24	550	98.7	920	4	AAW97652	Aay97652 Flt-1extr
25	550	98.7	927	4	AAW97653	Aay97653 Flk-1extr

26	541.5	97.2	331	4	AAB50893	Aab50893 Human Fas
27	513	92.1	104	7	ADC08900	Adc08900 FAS prote
28	427	76.7	84	4	AAW97654	Aay97654 Fas/Apo-1
29	425	76.3	84	2	AAW62178	Aaw62178 Fas-R pro
30	393	70.6	77	6	ADA49710	Ada49710 Death dom
31	386	69.3	77	5	ABG31494	Abg31494 Human Apo
32	352	63.2	68	3	AAW93611	Aaw93611 Human Fas
33	352	63.2	68	2	AAB26988	Aab26988 Human CD9
34	328	58.9	63	2	AAW00206	Aaw00206 Human Fas
35	278.5	50.0	327	2	AAR41688	Aar41688 Murine Fa
36	278.5	50.0	327	2	AAR78611	Aar78611 Murine Fa
37	278.5	50.0	327	2	AAR92530	Aar92530 mFas sequ
38	278.5	50.0	327	2	AAW86241	Aaw86241 Fas ligan
39	278.5	50.0	327	3	AAB19344	Aab19344 Amino aci
40	237	42.5	281	3	AAB26982	Aab26982 Human Fas
41	180.5	32.4	37	4	AAW72885	Aay72885 Death dom
42	86.5	15.5	1979	3	AAB18171	Aab18171 Plasmodi
43	80.5	14.5	67	3	AAW67948	Aay67948 Tumour ne
44	80.5	14.5	656	2	AAW04627	Aaw04627 Mouse rec
45	80.5	14.5	656	2	AAW80994	Aaw80994 Human rec

ALIGNMENTS

RESULT 1  
ABB81750  
ID ABB81750 standard; protein; 111 AA.

XX ABB81750;

AC ABB81750;

DT 10-SEP-2002 (first entry)

XX Tumour necrosis factor receptor Fas death domain (shorter sequence).

DE Tumour necrosis factor; receptor; TNFR-1; death domain; TNFR-1 DD; Fas;

KW Tumour necrosis factor; receptor; TNFR-1; death domain; TNFR-1 DD; Fas;

KW protein co-ordinate data.

XX Unidentified.

OS Unidentified.

XX Unidentified.

FT Key

FT Region

FT Region

FT Region

FT Region

FT Region

FT Region

FT Region

FT Region

FT Region

FT Region

FT Region

FT Region

FT Region

FT Region

Location/Qualifiers  
14..22  
/label= Alpha\_helix\_1  
25..34  
/label= Alpha\_helix\_2  
39..47  
/label= Alpha\_helix\_3  
57..68  
/label= Alpha\_helix\_4  
73..83  
/label= Alpha\_helix\_5  
89..101  
/label= Alpha\_helix\_6

US2002045578-A1.

18-APR-2002.

14-MAY-2001; 2001US-00854906.

22-MAY-2000; 2000US-0206215P.

(SUKI/) SUKITS S F.

(XUGG/) XU G.

(LINL/) LIN L.

(TELL/) TELLIEZ J.

(HSUS/) HSU S.

Sukits SF, Xu G, Lin L, Telliez J, Hsu S;

WPI; 2002-443412/47.

PT Solution comprising tumor necrosis factor receptor 1 death domain, useful

PT for identifying potential inhibitor of tumor necrosis factor receptor 1  
PT death domain.  
PS  
XX  
PS Example 1; Fig 4; 49pp; English.  
XX  
CC The sequence represents the tumour necrosis factor receptor Fas death  
CC domain (Fas DD). The invention relates to a novel solution comprising a  
CC tumour necrosis factor receptor 1 death domain. The solution is useful  
CC for identifying a potential inhibitor of TNFR-1 DD, for the design and  
CC selection of potent and selective inhibitors of TNF signalling pathways,  
CC and for generating a three-dimensional structure for an unknown molecule  
CC or molecular complex  
XX  
SQ Sequence 111 AA;  
  
Query Match 100.0%; Score 557; DB 5; Length 111;  
Best Local Similarity 100.0%; Pred. No. 2e-56;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 ETVAINLSVDLSKYITTIAGVMTLSQVKG FVRKNGVNEAKIDEIKNDNVQDTAEQKVQL 60  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1 ETVAINLSVDLSKYITTIAGVMTLSQVKG FVRKNGVNEAKIDEIKNDNVQDTAEQKVQL 60  
  
QY 61 LRNWHQLHGKKEAYDTLIKDLKKANLCTLAEKIQTIILKDITSDSENSNR 111  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
61 LRNWHQLHGKKEAYDTLIKDLKKANLCTLAEKIQTIILKDITSDSENSNR 111  
  
RESULT 2  
ABB81752  
ID ABB81752 standard; protein; 121 AA.  
XX  
AC ABB81752;  
XX  
DT 10-SEP-2002 (first entry)  
XX  
DE Tumour necrosis factor receptor Fas death domain (longer sequence).  
XX  
KW Tumour necrosis factor; receptor; TNFR-1; death domain; TNFR-1 DD; Fas;  
KW protein co-ordinate data.  
XX  
OS Unidentified.  
XX  
PN US2002045578-A1.  
XX  
PD 18-APR-2002.  
XX  
PF 14-MAY-2001; 2001US-00854906.  
XX  
PR 22-MAY-2000; 2000US-0206215P.  
XX  
PA (SUKI/) SUKITS S F.  
PA (XUGG/) XU G.  
PA (LINL/) LIN L.  
PA (TELL/) TELLIEZ J.  
PA (HSUS/) HSU S.  
XX  
PI Sukits SF, Xu G, Lin L, Telliez J, Hsu S;  
XX  
DR WPI; 2002-443412/47.  
XX  
XX  
PT Solution comprising tumor necrosis factor receptor 1 death domain, useful  
PT for identifying potential inhibitor of tumor necrosis factor receptor 1  
PT death domain.  
XX  
PS Example 1; Fig 7; 49pp; English.  
XX  
CC The sequence represents the tumour necrosis factor receptor Fas death  
CC domain (Fas DD). The invention relates to a novel solution comprising a  
CC tumour necrosis factor receptor 1 death domain. The solution is useful  
CC for identifying a potential inhibitor of TNFR-1 DD, for the design and  
CC selection of potent and selective inhibitors of TNF signalling pathways,  
CC and for generating a three-dimensional structure for an unknown molecule

CC or molecular complex  
XX  
SQ Sequence 121 AA;  
  
Query Match 100.0%; Score 557; DB 5; Length 121;  
Best Local Similarity 100.0%; Pred. No. 2.3e-56;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 ETVAINLSVDLSKYITTIAGVMTLSQVKG FVRKNGVNEAKIDEIKNDNVQDTAEQKVQL 60  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
2 ETVAINLSVDLSKYITTIAGVMTLSQVKG FVRKNGVNEAKIDEIKNDNVQDTAEQKVQL 61  
  
QY 61 LRNWHQLHGKKEAYDTLIKDLKKANLCTLAEKIQTIILKDITSDSENSNR 111  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
62 LRNWHQLHGKKEAYDTLIKDLKKANLCTLAEKIQTIILKDITSDSENSNR 112  
  
RESULT 3  
AAR76238  
ID AAR76238 standard; protein; 314 AA.  
XX  
AC AAR76238;  
XX  
DT 25-MAR-2003 (revised)  
DT 06-NOV-1995 (first entry)  
XX  
DE Fas-delta-TM.  
XX  
KW Fas-delta-TM; transmembrane deletion; apoptosis; antibody;  
KW adoptive immunotherapy; transgenic animal.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..16  
FT /label= Sig\_peptide  
XX  
PN WO9513701-A1.  
XX  
PD 26-MAY-1995.  
XX  
PF 15-NOV-1994; 94WO-US013173.  
XX  
PR 15-NOV-1993; 93US-00152443.  
XX  
PA (LXRB-) LXR BIOTECHNOLOGY INC.  
XX  
PI Barr PJ, Shapiro JP, Kiefer MC;  
XX  
DR WPI; 1995-200120/26.  
DR N-PSDB; AAQ93879.  
XX  
PT New nucleic acid encoding Fas protein without its trans-membrane region -  
PT and related vectors, transformed cells, transgenic animals, protein and  
PT antibodies, useful for control of Fas mediated apoptosis.  
XX  
PS Claim 9; Fig 3-1 to 3-4; 38pp; English.  
XX  
CC mRNA was obtd. from human lymphocytes and PCR was used to make cDNA  
CC specific for Fas-delta-TM (i.e. Fas lacking the transmembrane region)  
CC mRNA. The PCR product was ligated into pBluescript and the recombinant  
CC plasmid was used to transfect E. coli DH5-alpha cells. The insert  
CC sequence of pBluescript-Fas-delta-TM encoded the protein given in  
CC AAR76238. (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 314 AA;  
  
Query Match 100.0%; Score 557; DB 2; Length 314;  
Best Local Similarity 100.0%; Pred. No. 8.5e-56;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 ETVAINLSVDLSKYITTIAGVMTLSQVKG FVRKNGVNEAKIDEIKNDNVQDTAEQKVQL 60  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||



Db 197 ETVAINLSDVLSKYITTTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVQL 256

QY 61 LRNWHQLHGKKEAYDTLIKDLKKANLCTLAEKIQTIILKDITSDSENSNER 111

Db 257 LRNWHQLHGKKEAYDTLIKDLKKANLCTLAEKIQTIILKDITSDSENSNER 307

RESULT 4

AAR99682

ID AAR99682 standard; protein; 314 AA.

XX AC AAR99682;

XX DT 10-OCT-1996 (first entry)

XX DE Human Fas soluble antigen Fas dell.

XX KW Fas antigen; autoimmune disease; systemic lupus erythematosus; SLE;

XX KW angioimmunoblastic lymphadenopathy; AILD.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Peptide 1. .16

FT Protein 17. .314

FT Domain /label= Mat\_protein

FT /note= "soluble Fas dell antigen"

FT /label= Extracellular\_domain

FT /note= "the 5 C-terminal residues of the Fas antigen

FT extracellular domain are deleted in Fas dell"

FT 161. .171

FT Peptide /note= "preferred peptide from breakpoint region"

FT 164. .174

FT Peptide /note= "preferred peptide from breakpoint region"

FT 164. .173

FT Peptide /note= "preferred peptide from breakpoint region (claim

FT 4, page 132)"

FT 169. .314

FT Domain /label= Cytoplasmic\_domain

XX WO9620206-A1.

XX PD 04-JUL-1996.

XX PF 22-DEC-1995; 95WO-US017083.

XX PR 23-DEC-1994; 94US-00371263.

XX PA (UABR-) UAB RES FOUND.

XX PI Mountz JD, Liu C, Zhou T, Cheng J;

XX DR WPI; 1996-321796/32.

XX DR N-PSDB; AAT34527.

PT Natural, soluble form of Fas antigen secreted by human cells is result of

PT alternative mRNA processing - used to diagnose Fas-associated disease,

PT e.g. systemic lupus erythematosus.

XX Claim 4; Page 114-16; 152pp; English.

XX CC A natural, soluble Fas antigen variant (AAR99682), designated Fas dell,

CC and other Fas variants (AAR99683-85) are derived by alternative splicing

CC of Fas gene transcripts. A cDNA clone (AAT34527) coding for the variant

CC was obtd. from human peripheral blood mononuclear cells. The Fas dell

CC variant lacks the transmembrane domain of insoluble Fas antigen

CC (AAR99681). Recombinant dell variant, or fragments of it, can be

CC expressed in prokaryotic or eukaryotic (e.g. COS) cells. Detection of

CC increased levels of soluble forms of Fas antigen can be used to diagnose

CC autoimmune diseases, esp. systemic lupus erythematosus and

CC angioimmunoblastic lymphadenopathy

XX SQ Sequence 314 AA;

Query Match 100.0%; Score 557; DB 2; Length 314;

Best Local Similarity 100.0%; Pred. No. 8.5e-56;

Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETVAINLSDVLSKYITTTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVQL 60

Db 197 ETVAINLSDVLSKYITTTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVQL 256

QY 61 LRNWHQLHGKKEAYDTLIKDLKKANLCTLAEKIQTIILKDITSDSENSNER 111

Db 257 LRNWHQLHGKKEAYDTLIKDLKKANLCTLAEKIQTIILKDITSDSENSNER 307

RESULT 5

AAW98070

ID AAW98070 standard; protein; 314 AA.

XX AC AAW98070;

XX DT 21-JUN-1999 (first entry)

XX DE Soluble Fas receptor.

XX KW Fas receptor; Fas ligand; FasL; proinflammatory; immunosuppressive;

XX KW graft versus host disease; autoimmune disease; psoriasis;

XX KW rheumatoid arthritis; systemic lupus erythematosus; gene therapy.

XX OS Mammalia.

XX FH Key Location/Qualifiers

FT Peptide 1. .16

FT Protein 17. .314

FT /note= "signal peptide"

FT /note= "mature protein"

FT Misc-difference 109

FT /note= "encoded by GAA"

FT Modified-site 118

FT /note= "N-glycosylated"

XX WO9903999-A1.

XX PD 28-JAN-1999.

XX PF 16-JUL-1998; 98WO-US014771.

XX PR 17-JUL-1997; 97US-0052829P.

XX PA (UNMI ) UNIV MICHIGAN.

XX PI Nabel GJ, Chen J;

XX DR WPI; 1999-132243/11.

XX DR N-PSDB; AAX24878.

PT Inhibition of proinflammatory responses - using an agent which modulates

PT FasL stimulation, used for treating graft versus host disease or

PT autoimmune disease.

XX Disclosure; Fig 4B; 71pp; English.

XX CC This present sequence is a soluble Fas receptor. The invention provides a

CC method for inhibiting a proinflammatory response in a cell mixture by

CC administering an immunosuppressive agent which inhibits the

CC proinflammatory activity of Fas ligand (FasL). In some embodiments, an

CC FasL is coadministered with the immunosuppressive agent, and the cell

CC mixture comprises neutrophil cells. The method can be practised in vitro,

CC ex vivo or in vivo. Suitable immunosuppressive agents include antisense

CC molecules that inhibit endogenous FasL expression, soluble Fas receptors

CC or variants, ribozymes that inhibit the endogenous expression of FasL,

CC drugs that inhibit FasL signalling, agents that induce the endogenous

CC expression of transforming growth factor (TGF)-beta, and polynucleotides  
CC coding for an immunosuppressive agent such as TGF-beta. The method can be  
CC used for treating diseases associated with an undesired FasL-mediated  
CC proinflammatory response, e.g. graft versus host disease, or an  
CC autoimmune disease such as systemic lupus erythematosus, rheumatoid  
CC arthritis and psoriasis. The invention also provides a method for  
CC identifying agents which modulate FasL stimulation of a proinflammatory  
CC response  
XX  
SQ Sequence 314 AA;  
  
Query Match 100.0%; Score 557; DB 2; Length 314;  
Best Local Similarity 100.0%; Pred. No. 8.5e-56;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 ETVAINLSVDLSKYITTTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVQL 60  
Db 197 ETVAINLSVDLSKYITTTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVQL 256  
QY 61 LRNWHQLHGKKEAYDTLIKDLKKANLCTLAEKIQTIILKDITSDSENSNFR 111  
Db 257 LRNWHQLHGKKEAYDTLIKDLKKANLCTLAEKIQTIILKDITSDSENSNFR 307  
  
RESULT 6  
AAR28084  
ID AAR28084 standard; protein; 335 AA.  
XX  
AC AAR28084;  
XX  
DT 25-MAR-2003 (revised)  
DT 12-MAR-1993 (first entry)  
XX  
DE Human cell surface antigen.  
DE  
KW Fas antigen; apoptosis; pF58; NGFR/TNFR family.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..16  
FT /label= signal  
FT Protein 17..335  
FT /label= Fas\_antigen  
FT Domain 17..173  
FT /label= extracellular  
FT /note= "cysteine-rich"  
FT Modified-site 118..120  
FT /label= N-glycosylation\_site  
FT /note= "putative"  
FT Modified-site 136..138  
FT /label= N-glycosylation\_site  
FT /note= "putative"  
FT Domain 174..190  
FT /label= transmembrane  
FT Domain 191..335  
FT /label= cytoplasmic  
XX  
PN EP510691-A1.  
XX  
PD 28-OCT-1992.  
XX  
PF 24-APR-1992; 92EP-00107060.  
XX  
PR 26-APR-1991; 91JP-00125234.  
XX  
PA (OSAB-) OSAKA BIOSCIENCE INST.  
XX  
PI Nagata S, Itoh N, Yonehara S;  
XX  
DR WPI; 1992-358914/44.  
DR N-PSDB; AAQ29959.  
XX

PT DNA encoding human cell surface antigen - used to clarify apoptosis  
PT mechanism of various types of cell, and to prepare monoclonal antibodies  
PT that react with tumour cells expressing Fas.  
XX  
PS Claim 3; Fig 1 and 2; 27pp; English.  
XX  
CC The Fas antigen is implicated in apoptosis. A cDNA clone encoding the  
CC antigen was isolated (pF58) and the amino acid sequence of Fas was  
CC deduced from it. The mature protein has a calculated mol.wt. of 36,000  
CC and is a member of the NGFR/TNFR family of cell-surface membrane  
CC proteins. The inventors claim a protein comprising at least the  
CC extracellular domain of Fas antigen. (Updated on 25-MAR-2003 to correct  
CC PN field.)  
XX  
SQ Sequence 335 AA;  
  
Query Match 100.0%; Score 557; DB 2; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.3e-56;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 ETVAINLSVDLSKYITTTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVQL 60  
Db 218 ETVAINLSVDLSKYITTTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVQL 277  
QY 61 LRNWHQLHGKKEAYDTLIKDLKKANLCTLAEKIQTIILKDITSDSENSNFR 111  
Db 278 LRNWHQLHGKKEAYDTLIKDLKKANLCTLAEKIQTIILKDITSDSENSNFR 328  
  
RESULT 7  
AAR78606  
ID AAR78606 standard; protein; 335 AA.  
XX  
AC AAR78606;  
XX  
DT 19-FEB-1996 (first entry)  
XX  
DE Human Fas protein.  
XX  
KW Plasmid pF58; human Fas cDNA; soluble membrane protein;  
KW antibody production; diseases; treatment; prevention.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..16  
FT /label= sig\_peptide  
FT Peptide 17..335  
FT /label= mat\_peptide  
XX  
PN JP07115988-A.  
XX  
PD 09-MAY-1995.  
XX  
PF 26-OCT-1993; 93JP-00267644.  
XX  
PR 26-OCT-1993; 93JP-00267644.  
XX  
PA (NISB ) JAPAN TOBACCO INC.  
XX  
DR WPI; 1995-202847/27.  
DR N-PSDB; AAQ95297.  
XX  
PT Preparation of soluble membrane proteins - for their use in antibody  
PT production for the treatment and prevention of related diseases.  
XX  
PS Example 1; Page 15-17; 51pp; Japanese.  
XX  
CC AAR78606 (human Fas protein) is encoded by the plasmid pF58 which  
CC contains hFas cDNA. The plasmid was used in the construction of an  
CC expression vector for the prodn. of recombinant soluble membrane  
CC proteins. The proteins can be used in antibody prodn. for the treatment  
CC and prevention of related diseases

```
XX SQ Sequence 335 AA;
Query Match 100.0%; Score 557; DB 2; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.3e-56;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETVAINLSVDLSKYITTIAGVMTLSQVKGFVRKNGVNEAKIDEIKNDNVQDTAEQKVQL 60
Db 218 ETVAINLSVDLSKYITTIAGVMTLSQVKGFVRKNGVNEAKIDEIKNDNVQDTAEQKVQL 277

QY 61 LRNWHQLHGKKEAYDTLIKDLKKANLCTLAEKIQTIILKDITSDSENSNFR 111
Db 278 LRNWHQLHGKKEAYDTLIKDLKKANLCTLAEKIQTIILKDITSDSENSNFR 328

RESULT 8
AAR99681
ID AAR99681 standard; protein; 335 AA.
XX
AC AAR99681;
XX
DT 10-OCT-1996 (first entry)
XX
DE Human Fas antigen.
XX
KW Fas antigen; autoimmune disease; systemic lupus erythematosus; SLE;
KW angioimmunoblastic lymphadenopathy; AILD.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..16
FT /label= Sig_peptide
FT Protein 17..335
FT /label= Mat_protein
FT Domain 17..173
FT /label= Extracellular_domain
FT Domain 174..190
FT /label= Transmembrane_domain
FT Domain 191..335
FT /label= Cytoplasmic_tail
XX
PN WO9620206-A1.
XX
PD 04-JUL-1996.
XX
PF 22-DEC-1995; 95WO-US017083.
XX
PR 23-DEC-1994; 94US-00371263.
XX
PA (UABR-) UAB RES FOUND.
XX
PI Mountz JD, Liu C, Zhou T, Cheng J;
XX WPI; 1996-321796/32.
DR N-PSDB; AAT34526.
XX
PT Natural, soluble form of Fas antigen secreted by human cells is result of
PT alternative mRNA processing - used to diagnose Fas-associated disease,
PT e.g. systemic lupus erythematosus.
XX
PS Disclosure; Page 109-111; 152pp; English.
XX
CC A cDNA clone (AAT34526) codes for a membrane receptor-like protein, Fas
CC antigen (AAR99681). It was isolated from cDNA derived from the peripheral
CC blood mononuclear cells of systemic lupus erythematosus (SLE) and
CC angioimmunoblastic lymphadenopathy (AILD) patients. 4 Soluble variants
CC (AAR99682-85) were identified of the Fas antigen. These arose by
CC alternative splicing of Fas gene transcripts. The Fas variants were
CC present at higher levels in SLE and AILD patients than the non-soluble
CC Fas antigen
XX
```

```
SQ Sequence 335 AA;
Query Match 100.0%; Score 557; DB 2; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.3e-56;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETVAINLSVDLSKYITTIAGVMTLSQVKGFVRKNGVNEAKIDEIKNDNVQDTAEQKVQL 60
Db 218 ETVAINLSVDLSKYITTIAGVMTLSQVKGFVRKNGVNEAKIDEIKNDNVQDTAEQKVQL 277

QY 61 LRNWHQLHGKKEAYDTLIKDLKKANLCTLAEKIQTIILKDITSDSENSNFR 111
Db 278 LRNWHQLHGKKEAYDTLIKDLKKANLCTLAEKIQTIILKDITSDSENSNFR 328

RESULT 9
AAR92528
ID AAR92528 standard; protein; 335 AA.
XX
AC AAR92528;
XX
DT 06-SEP-1996 (first entry)
XX
DE hFas from plasmid pCEV4/hFas.
XX
KW Fas; antigen; immunoassay; monoclonal antibody; autoimmune disease; SLE;
KW rheumatoid arthritis; serum; systemic lupus erythematosus.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1..16
FT /note= "hFas signal peptide"
FT Protein 17..335
FT /note= "mature hFas"
XX
PN WO9601277-A1.
XX
PD 18-JAN-1996.
XX
PF 03-MAR-1995; 95WO-JP000349.
XX
PR 06-JUL-1994; 94JP-00154706.
PR 14-FEB-1995; 95JP-00025637.
XX
PA (MEDI-) MEDICAL & BIOLOGICAL LAB CO LTD.
PA (NISE ) JAPAN TOBACCO INC.
XX
PI Yonehara S, Noguchi J, Hachiya T;
XX WPI; 1996-087635/09.
DR N-PSDB; AAT16303.
XX
PT Immunoassay method for soluble Fas antigen in body fluids - for diagnosis
PT of autoimmune diseases such as rheumatoid arthritis and systemic lupus
PT erythematosus.
XX
PS Example 8; Page 49-52; 124pp; Japanese.
XX
CC This sequence represents the sequence for the human Fas antigen contained
CC within the plasmid pCEV4/hFas. The soluble Fas antigen is included in the
CC immunoassay kit of the invention. The kit is for the assay of soluble Fas
CC antigen and contains an immobilised anti-soluble Fas monoclonal antibody,
CC as well as the standard soluble Fas antigen represented by this sequence.
CC The assay is simple and has high accuracy, high sensitivity, and is
CC capable of assaying a number of different specimens at the same time. The
CC immunoassay is used on biological samples (such as serum) and is useful
CC for diagnosis of autoimmune diseases such as rheumatoid arthritis or
CC systemic lupus erythematosus (SLE)
XX
SQ Sequence 335 AA;
Query Match 100.0%; Score 557; DB 2; Length 335;
```

Best Local Similarity 100.0%; Pred. No. 9.3e-56;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETVAINLSDVDLSKYITTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVQL 60  
DB 218 ETVAINLSDVDLSKYITTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVQL 277

QY 61 LRNWHQLHGKKEAYDTLIKDLKKANLCTLAEKIQTIILKDITSDSENSNFR 111  
DB 278 LRNWHQLHGKKEAYDTLIKDLKKANLCTLAEKIQTIILKDITSDSENSNFR 328

RESULT 10  
AAW50289  
ID AAW50289 standard; protein; 335 AA.  
XX  
AC AAW50289;  
XX  
DT 16-JUL-1998 (first entry)  
XX  
DE Human Fas antigen.  
XX  
KW Human; Fas antigen; derivative; apoptosis regulation; gene therapy;  
KW treatment; diabetes; arthritis; lupus; hepatitis; influenza; HIV;  
KW apoptosis modulation.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1. .16  
FT /label= sig\_peptide  
FT Peptide 17. .335  
FT /label= mat\_peptide  
FT Region 17. .173  
FT /note= "claimed fragment"  
XX  
PN WO9742319-A1.  
XX  
PD 13-NOV-1997.  
XX  
PF 01-MAY-1997; 97WO-JP001502.  
XX  
PR 02-MAY-1996; 96JP-00135760.  
XX  
PA (MOCH ) MOCHIDA PHARM CO LTD.  
PA (OSAB-) OSAKA BIOSCIENCE INST.  
XX  
PI Nakamura N, Nagata S;  
XX  
DR WPI; 1997-558981/51.  
DR N-PSDB; AAV07002.  
XX  
PT Fas antigen derivative containing modified extracellular region - has low  
PT antigenicity, promotes apoptosis and is useful in treatment of viral and  
PT other diseases.  
XX  
PS Claim 2; Fig 1-2; 102pp; Japanese.  
XX  
CC The present sequence was used in the development of novel Fas antigen  
CC derivatives, which contain a Fas antigen extracellular region lacking one  
CC or more amino acid residues in the region from the amino-terminal to (but  
CC excluding) the 1st cysteine residue (preferably at least 29 residues are  
CC deleted). The derivatives are effective regulators of apoptosis and can  
CC be used (either by administration of the polypeptide, or by the use of  
CC the coding DNA in gene therapy) to treat a range of diseases, e.g.  
CC diabetes, arthritis, lupus and in particular viral diseases such as  
CC hepatitis, influenza and HIV, by modulating apoptosis of virus-infected  
CC cells  
XX  
SQ Sequence 335 AA;

Query Match 100.0%; Score 557; DB 2; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.3e-56;

Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETVAINLSDVDLSKYITTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVQL 60  
DB 218 ETVAINLSDVDLSKYITTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVQL 277

QY 61 LRNWHQLHGKKEAYDTLIKDLKKANLCTLAEKIQTIILKDITSDSENSNFR 111  
DB 278 LRNWHQLHGKKEAYDTLIKDLKKANLCTLAEKIQTIILKDITSDSENSNFR 328

RESULT 11  
AAW49104  
ID AAW49104 standard; protein; 335 AA.  
XX  
AC AAW49104;  
XX  
DT 27-AUG-2003 (revised)  
DT 18-NOV-1998 (first entry)  
XX  
DE Fas protein.  
XX  
KW Fas protein; CD8+ T-lymphocyte killer cell; TK; Fas-ligand; FasL;  
KW CD4+ cell; apoptosis; lymphocyte; human immunodeficiency virus; HIV;  
KW simian immunodeficiency virus; SIV; cytotoxic T lymphocyte; CTL;  
KW prophylactic; AIDS.  
XX  
OS Mammalia.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1. .16  
FT /note= "Signal peptide"  
FT Protein 17. .335  
FT /note= "Fas protein"  
FT Region 17. .172  
FT /note= "The portion of a Fas protein which can be fused  
FT to a Fc polypeptide to form a Fas-Fc fusion protein"  
XX  
PN WO9835692-A1.  
XX  
PD 20-AUG-1998.  
XX  
PF 17-FEB-1998; 98WO-GB000485.  
XX  
PR 17-FEB-1997; 97GB-00003276.  
XX  
PA (ISIS-) ISIS INNOVATION LTD.  
XX  
PI Screaton GR, Xu X;  
XX  
DR WPI; 1998-456867/39.  
DR N-PSDB; AAV32993.  
XX  
PT Reducing CD8+ lymphocyte apoptosis to treat e.g. immunodeficiency  
PT diseases - by interfering with interaction of Fas with Fas-ligand  
PT expressed on activated CD4+ cells, e.g. cells infected with HIV.  
XX  
PS Disclosure; Fig 7; 71pp; English.  
XX  
CC The present sequence represents a Fas protein sequence used in the method  
CC of the invention. The method is concerned with reducing depletion of  
CC activated Fas-expressing CD8+ T-lymphocyte killer (TK) cells in an immune  
CC cell population which also comprises of Fas-ligand (FasL)-expressing  
CC activated CD4+ cells. It involves contacting this immune cell population  
CC with an effective amount of an agent (e.g. a soluble Fas-Fc fusion  
CC protein) which would interfere with the interaction between Fas and FasL.  
CC Therefore, the method is useful for identifying suitable agents which can  
CC reduce depletion of activated Fas-expressing CD8+ TK cells in immune cell  
CC populations. Also claimed is the use of the agent in the manufacture of  
CC therapeutic compositions. Apoptosis of lymphocytes can be triggered by  
CC the interaction of the cell surface receptor Fas and its ligand FasL. By  
CC interfering with this interaction, the method described and its  
CC preparations can prevent apoptosis of CD8+ TK lymphocytes caused by





```
RESULT 14
AAB36267
ID AAB36267 standard; protein; 335 AA.
XX
AC AAB36267;
XX
DT 20-FEB-2001 (first entry)
XX
DE Human Fas receptor.
XX
KW Human; death domain containing receptor; DR3-V1; cancer;
KW autoimmune disorder; inflammation; cardiovascular disorder; infection;
KW neurodegenerative disease; angiogenesis.
XX
OS Homo sapiens.
XX
PN WO200064465-A1.
XX
PD 02-NOV-2000.
XX
PF 21-APR-2000; 2000WO-US010741.
XX
PR 22-APR-1999; 99US-0130488P.
PR 28-MAY-1999; 99US-0136741P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA (UNMI ) UNIV MICHIGAN.
PA (YUGG/) YU G.
PA (NIJJ/) NI J.
PA (GENT/) GENTZ R L.
PA (DILL/) DILLON P J.
PA (DIXI/) DIXIT V M.
XX
PI Yu G, Ni J, Gentz RL, Dillon PJ, Dixit VM;
XX
XX WPI; 2000-687263/67.
XX
XX Treating graft-versus-host disease, cancer, immunodeficiency or an
PT autoimmune disease comprising administering an antibody to Death Domain
PT Containing Receptor proteins and a second therapeutic agent.
XX
XX Disclosure; Fig 3; 273pp; English.
XX
CC The present invention provides the protein and coding sequences for two
CC death domain containing receptors, designated DR3 and DR3-V1. These
CC receptors are involved in apoptosis, and the sequences given can be used
CC in the treatment of cancers, infections, cardiovascular diseases such as
CC arrhythmias, ischaemia, aneurysms, arterial occlusive diseases, embolisms
CC and congenital heart defects, neurodegenerative diseases including
CC Alzheimer's and Parkinson's diseases, autoimmune disease such as multiple
CC sclerosis, arthritis, diabetes, Graves' disease, asthma and psoriasis,
CC and to promote angiogenesis and wound healing
XX
SQ Sequence 335 AA;
Query Match 100.0%; Score 557; DB 3; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.3e-56;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ETVAINLSDVDLSKYITTIAGVMTLSQVKG FVRKNGVNEAKIDEIKNDNVQDTAEQKVQL 60
Db 218 ETVAINLSDVDLSKYITTIAGVMTLSQVKG FVRKNGVNEAKIDEIKNDNVQDTAEQKVQL 277
QY 61 LRNWHQLHGKKEAYDTLIKDLKKANLCTLAEKIQTIIILKDITSDSENSNFR 111
Db 278 LRNWHQLHGKKEAYDTLIKDLKKANLCTLAEKIQTIIILKDITSDSENSNFR 328
RESULT 15
AAB50517
ID AAB50517 standard; protein; 335 AA.
XX
```

```
AC AAB50517;
XX
DT 15-MAR-2001 (first entry)
XX
DE Human tumour necrosis factor receptor FAS protein SEQ ID NO:7.
XX
KW Human; tumour necrosis factor receptor 5; TRID; TNFR-5; TR5; nootropic;
KW TRAIL receptor without intracellular domain; diagnosis; cytostatic;
KW tumour necrosis factor related apoptosis inducing ligand; vasotrophic;
KW immunosuppressive; neuroprotective; antiviral; antiinflammatory;
KW anticonvulsant; antiparasitic; cardiant; anti-HIV; antiparkinsonian;
KW gene therapy; restenosis; graft versus host disease; tumour; cancer;
KW apoptotic cell death related disease; autoimmune disorder;
KW cardiovascular disorder; viral infection.
XX
OS Homo sapiens.
XX
PN WO200071150-A1.
XX
PD 30-NOV-2000.
XX
PF 18-MAY-2000; 2000WO-US013515.
XX
PR 20-MAY-1999; 99US-0135164P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Wei Y, Ruben SM, Gentz RL, Ni J;
XX
XX WPI; 2001-041051/05.
XX
XX Nucleic acid encoding a TRID polypeptide, also referred to as tumor
PT necrosis factor receptor 5, useful in the diagnosis, treatment or
PT prevention of cancer, autoimmune disorders and viral infection.
XX
PS Disclosure; Fig 2; 285pp; English.
XX
CC The present invention describes the human TRID protein (tumour necrosis
CC factor (TNF) related apoptosis inducing ligand (TRAIL) receptor without
CC intracellular domain, also referred to as tumour necrosis factor receptor
CC 5 (TNFR-5 or TR5)). TRID has cytostatic, immunosuppressive, nootropic,
CC neuroprotective, antiviral, antiinflammatory, anticonvulsant,
CC antiparasitic, cardiant, anti-HIV, antiparkinsonian and vasotropic
CC activities, and can be used in gene therapy. The TRID polynucleotides are
CC useful for detecting complementary polynucleotides. TRID proteins and
CC polynucleotides are useful in the treatment of tumours, resistance to
CC parasite, bacteria and viruses, restenosis and graft versus host disease.
CC They are also useful for inducing proliferation of T-cells, endothelial
CC cells and certain haematopoietic cells, to regulate antiviral responses
CC and to prevent certain autoimmune diseases after stimulation of TRID by
CC an agonist or TRAIL binding facilitator. The antibodies which bind TRID
CC polypeptides are useful for treating and/or preventing diseases
CC associated with increased or decreased apoptotic cell death. The TRID
CC polynucleotides, proteins, antibodies, agonists and antagonists are
CC useful in the diagnosis, treatment or prevention of: (a) cancer; (b)
CC autoimmune disorders; (c) diseases associated with increased apoptosis;
CC (d) cardiovascular disorders; and (e) viral infection. The present
CC sequence represents a tumour necrosis factor receptor used in comparison
CC with TRID in the exemplification of the present invention
XX
SQ Sequence 335 AA;
Query Match 100.0%; Score 557; DB 4; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.3e-56;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ETVAINLSDVDLSKYITTIAGVMTLSQVKG FVRKNGVNEAKIDEIKNDNVQDTAEQKVQL 60
Db 218 ETVAINLSDVDLSKYITTIAGVMTLSQVKG FVRKNGVNEAKIDEIKNDNVQDTAEQKVQL 277
QY 61 LRNWHQLHGKKEAYDTLIKDLKKANLCTLAEKIQTIIILKDITSDSENSNFR 111
Db 278 LRNWHQLHGKKEAYDTLIKDLKKANLCTLAEKIQTIIILKDITSDSENSNFR 328
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Job time : 49.521 secs

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OM protein - protein search, using sw model

Run on: June 1, 2004, 14:41:22 ; Search time 13.9581 Seconds  
(without alignments)  
410.549 Million cell updates/sec

Title: US-09-854-906-9  
Perfect score: 557  
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Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
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2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	557	100.0	314	1	US-08-444-231-19
2	557	100.0	314	1	US-08-152-443A-19
3	557	100.0	314	5	PCT-US95-17083-4
4	557	100.0	335	2	US-08-219-237B-2
5	557	100.0	335	2	US-08-409-338-1
6	557	100.0	335	3	US-08-815-469-6
7	557	100.0	335	3	US-09-290-640-2
8	557	100.0	335	3	US-09-006-353A-7
9	557	100.0	335	3	US-08-468-560C-2
10	557	100.0	335	4	US-09-180-100-20
11	557	100.0	335	4	US-09-565-918-3
12	557	100.0	335	4	US-09-573-986-7
13	557	100.0	335	4	US-09-665-615B-2
14	557	100.0	335	5	PCT-US95-17083-2
15	557	100.0	669	4	US-09-013-895A-3
16	557	100.0	669	4	US-09-448-868-3
17	541.5	97.2	331	3	US-09-086-483A-3
18	541.5	97.2	331	4	US-09-580-212-3
19	541.5	97.2	331	4	US-09-769-402-3
20	431	77.4	85	3	US-09-042-785A-26
21	425	76.3	84	4	US-09-069-827A-119
22	393	70.6	77	4	US-08-828-683A-24
23	361	64.8	70	4	US-09-159-277A-5
24	352	63.2	68	4	US-09-527-236A-22
25	352	63.2	68	4	US-09-756-854-22
26	328	58.9	63	4	US-08-894-626-1
27	278.5	50.0	327	3	US-09-290-640-66

28	278.5	50.0	327	4	US-09-665-615B-66	Sequence 66, Appl
29	237	42.5	45	2	US-08-219-237B-10	Sequence 10, Appl
30	237	42.5	281	4	US-09-527-236A-3	Sequence 3, Appli
31	237	42.5	281	4	US-09-756-854-3	Sequence 3, Appli
32	212	38.1	40	1	US-08-444-005-27	Sequence 27, Appl
33	182	32.7	70	4	US-09-159-277A-4	Sequence 4, Appli
34	167	30.0	41	1	US-08-444-005-33	Sequence 33, Appl
35	137	24.6	40	1	US-08-444-005-26	Sequence 26, Appl
36	122	21.9	25	1	US-08-444-005-21	Sequence 21, Appl
37	82	14.7	261	4	US-09-634-238-420	Sequence 420, App
38	80.5	14.5	656	1	US-08-444-005-15	Sequence 15, Appl
39	80.5	14.5	656	4	US-09-069-023-28	Sequence 28, Appl
40	80.5	14.5	656	4	US-09-345-473E-30	Sequence 30, Appl
41	78.5	14.1	77	3	US-08-995-159-7	Sequence 7, Appli
42	78.5	14.1	77	4	US-09-545-605-7	Sequence 7, Appli
43	78.5	14.1	87	3	US-09-042-785A-29	Sequence 29, Appl
44	78.5	14.1	671	3	US-09-132-118-2	Sequence 2, Appli
45	78.5	14.1	671	4	US-09-345-473E-29	Sequence 29, Appl

ALIGNMENTS

RESULT 1  
US-08-444-231-19  
; Sequence 19, Application US/08444231  
; Patent No. 5652210  
; GENERAL INFORMATION:  
; APPLICANT: BARR, PHILIP J.  
; APPLICANT: SHAPIRO, JOHN P.  
; APPLICANT: KIEFER, MICHAEL C.  
; TITLE OF INVENTION: NOVEL FAS PROTEIN AND METHODS OF USE  
; TITLE OF INVENTION: THEREOF  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/444,231  
; FILING DATE: 18-MAY-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/152,443  
; FILING DATE: 15-NOV-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: LEHNHARDT, SUSAN K.  
; REGISTRATION NUMBER: 33,943  
; REFERENCE/DOCKET NUMBER: 23647-20006.00  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 813-5600  
; TELEFAX: (415) 494-0792  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 314 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-444-231-19

Query Match 100.0%; Score 557; DB 1; Length 314;  
Best Local Similarity 100.0%; Pred. No. 4.5e-56;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



[illegible]

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RESULT 2
US-08-152-443A-19
; Sequence 19, Application US/08152443A
; Patent No. 5663070
; GENERAL INFORMATION:
; APPLICANT: BARR, PHILIP J.
; APPLICANT: SHAPIRO, JOHN P.
; APPLICANT: KIEFER, MICHAEL C.
; TITLE OF INVENTION: NOVEL FAS PROTEIN AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/152.443A

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Query Match      100.0%; Score 557; DB 1; Length 314;
Best Local Similarity 100.0%; Pred. No. 4.5e-56;
Matches 111: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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[illegible]

RESULT 3  
PCT-US95-17083-4  
; Sequence 4, Application PC/TUS9517083  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: SECRETED HUMAN FAS ANTIGEN  
; NUMBER OF SEQUENCES: 16  
; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: PCT/US95/17083
; FILING DATE: CONCURRENTLY HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/371,263
; FILING DATE: 23-DEC-1994
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 314 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; PCT-US95-17083-4

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Query Match      100.0%; Score 557; DB 5; Length 314;
Best Local Similarity 100.0%; Pred. NO. 4.5e-56;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 4  
US-08-219-237B-2  
; Sequence 2, Application US/08219237B  
; Patent No. 5874546  
; GENERAL INFORMATION:  
; APPLICANT: NAGATA, Shigekazu  
; APPLICANT: ITOH, Naoto  
; APPLICANT: YONEHARA, Shin  
; TITLE OF INVENTION: DNA Coding for Human Cell Surface Antigen  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: James W. Hellwege  
; STREET: P.O. Box 2266 Eads Station  
; CITY: Arlington  
; STATE: Virginia  
; COUNTRY: USA  
; ZIP: 22202

Query Match 100.0%; Score 557; DB 2; Length 335;  
Best Local Similarity 100.0%; Pred. NO. 5e-56;  
Matches 111: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 218 ETVAINLSDVLSKYITTTIAGVMTLSQVKG FVRKNGVNEAKIDEIKNDNVQDTAEQKVQL 277  
QY 61 LRNWHQLHGKKEAYDTLIKDLKKANLCTLAEKIQTIILKDITSDSENSNFR 111  
Db 278 LRNWHQLHGKKEAYDTLIKDLKKANLCTLAEKIQTIILKDITSDSENSNFR 328

RESULT 5  
US-08-409-338-1  
; Sequence 1, Application US/08409338  
; Patent No. 5891434  
; GENERAL INFORMATION:  
; APPLICANT: Krammer, Peter H.  
; APPLICANT: Debatin, Klaus-Michael  
; APPLICANT: Trauth, Bernhard C.  
; APPLICANT: Behrmann, Iris  
; APPLICANT: Dhein, Jens  
; APPLICANT: Klas, Christiane  
; APPLICANT: M ller, Peter  
; APPLICANT: Falk, Werner  
; APPLICANT: Oehm Alexander  
; APPLICANT: Daniel, Peter T.  
; TITLE OF INVENTION: Monoclonal Antibodies to the APO-1 Antigen  
; NUMBER OF SEQUENCES: 1  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington, MA 02173  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02173

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/409,338  
; FILING DATE:

CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/260,644  
; FILING DATE: 16-JUN-1994  
; APPLICATION NUMBER: US 07/691,016  
; FILING DATE: 17-JUN-1991  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brook, David E.  
; REGISTRATION NUMBER: 22,592  
; REFERENCE/DOCKET NUMBER: CTR89-35A2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-861-6240  
; TELEFAX: 617-861-9540  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 335 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
US-08-409-338-1

Query Match 100.0%; Score 557; DB 2; Length 335;  
Best Local Similarity 100.0%; Pred. No. 5e-56;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETVAINLSDVLSKYITTTIAGVMTLSQVKG FVRKNGVNEAKIDEIKNDNVQDTAEQKVQL 60  
Db 218 ETVAINLSDVLSKYITTTIAGVMTLSQVKG FVRKNGVNEAKIDEIKNDNVQDTAEQKVQL 277  
QY 61 LRNWHQLHGKKEAYDTLIKDLKKANLCTLAEKIQTIILKDITSDSENSNFR 111  
Db 278 LRNWHQLHGKKEAYDTLIKDLKKANLCTLAEKIQTIILKDITSDSENSNFR 328

RESULT 6  
US-08-815-469-6  
; Sequence 6, Application US/08815469  
; Patent No. 6153402  
; GENERAL INFORMATION:  
; APPLICANT: Yu, Guo-Liang  
; APPLICANT: Ni, Jian  
; APPLICANT: Dixit, Vishva  
; APPLICANT: Gentz, Reiner L.  
; APPLICANT: Dillon, Patrick J.  
; TITLE OF INVENTION: Death Domain Containing Receptors  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.  
; STREET: 1100 New York Ave., NW, Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/815,469  
; FILING DATE: HEREWITH  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: No. 6153402 Yet Assigned  
; FILING DATE: 06-FEB-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/028,711  
; FILING DATE: 17-OCT-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/013,285  
; FILING DATE: 12-MAR-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Steffe, Eric K.  
; REGISTRATION NUMBER: 36,688  
; REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 335 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: not relevant  
; MOLECULE TYPE: protein  
US-08-815-469-6

Query Match 100.0%; Score 557; DB 3; Length 335;  
Best Local Similarity 100.0%; Pred. No. 5e-56;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETVAINLSDVLSKYITTTIAGVMTLSQVKG FVRKNGVNEAKIDEIKNDNVQDTAEQKVQL 60  
Db 218 ETVAINLSDVLSKYITTTIAGVMTLSQVKG FVRKNGVNEAKIDEIKNDNVQDTAEQKVQL 277  
QY 61 LRNWHQLHGKKEAYDTLIKDLKKANLCTLAEKIQTIILKDITSDSENSNFR 111  
Db 278 LRNWHQLHGKKEAYDTLIKDLKKANLCTLAEKIQTIILKDITSDSENSNFR 328

RESULT 7  
US-09-290-640-2  
; Sequence 2, Application US/09290640  
; Patent No. 6204055  
; GENERAL INFORMATION:  
; APPLICANT: Dean, Nicholas M.

APPLICANT: Marcusson, Eric G.  
TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling  
FILE REFERENCE: ISPH-0351  
CURRENT APPLICATION NUMBER: US/09/290,640  
CURRENT FILING DATE: 1999-04-12  
NUMBER OF SEQ ID NOS: 85  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 335  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-290-640-2

Query Match 100.0%; Score 557; DB 3; Length 335;  
Best Local Similarity 100.0%; Pred. No. 5e-56;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETVAINLSDVLSKYITTTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVQL 60  
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Db 218 ETVAINLSDVLSKYITTTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVQL 277  
QY 61 LRNWHQLHGKKEAYDTLLKDLKANLCTLAEKIQTIILKDITSDSENSNFR 111  
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Db 278 LRNWHQLHGKKEAYDTLLKDLKANLCTLAEKIQTIILKDITSDSENSNFR 328

RESULT 8  
US-09-006-353A-7  
Sequence 7, Application US/09006353A  
Patent No. 6261801  
GENERAL INFORMATION:  
APPLICANT: WEI, YING-FEI  
APPLICANT: YU, GUO-LIANG  
APPLICANT: GENTZ, REINER  
APPLICANT: RUBEN, STEVEN  
TITLE OF INVENTION: TUMOR NECROSIS FACTOR RECEPTOR 5  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HUMAN GENOME SCIENCES, INC.  
STREET: 9410 KEY WEST AVENUE  
CITY: ROCKVILLE  
STATE: MD  
COUNTRY: US  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/006,353A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: BROOKES, ANDERS A  
REGISTRATION NUMBER: 36,373  
REFERENCE/DOCKET NUMBER: PF341  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (301) 309-8504  
TELEFAX: (301) 309-8512  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 335 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-006-353A-7

Query Match 100.0%; Score 557; DB 3; Length 335;  
Best Local Similarity 100.0%; Pred. No. 5e-56;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETVAINLSDVLSKYITTTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVQL 60  
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Db 218 ETVAINLSDVLSKYITTTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVQL 277  
QY 61 LRNWHQLHGKKEAYDTLLKDLKANLCTLAEKIQTIILKDITSDSENSNFR 111  
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Db 278 LRNWHQLHGKKEAYDTLLKDLKANLCTLAEKIQTIILKDITSDSENSNFR 328

RESULT 9  
US-08-468-560C-2  
Sequence 2, Application US/08468560C  
Patent No. 6270998  
GENERAL INFORMATION:  
APPLICANT: NAGATA, Shigekazu  
APPLICANT: ITOH, Naoto  
APPLICANT: YONEHARA, Shin  
TITLE OF INVENTION: DNA CODING FOR HUMAN CELL SURFACE  
TITLE OF INVENTION: ANTIGEN  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP.  
STREET: P.O. BOX 747  
CITY: FALLS CHURCH  
STATE: VA  
COUNTRY: USA  
ZIP: 22040-0747  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/468,560C  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MURPHY JR., GERLAD M.  
REGISTRATION NUMBER: 28,977  
REFERENCE/DOCKET NUMBER: 20-4393P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-205-8000  
TELEFAX: 703-205-8050  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 335 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-468-560C-2

Query Match 100.0%; Score 557; DB 3; Length 335;  
Best Local Similarity 100.0%; Pred. No. 5e-56;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETVAINLSDVLSKYITTTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVQL 60  
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Db 218 ETVAINLSDVLSKYITTTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVQL 277  
QY 61 LRNWHQLHGKKEAYDTLLKDLKANLCTLAEKIQTIILKDITSDSENSNFR 111  
|||||  
Db 278 LRNWHQLHGKKEAYDTLLKDLKANLCTLAEKIQTIILKDITSDSENSNFR 328

RESULT 10  
US-09-180-100-20  
Sequence 20, Application US/09180100  
Patent No. 6306395  
GENERAL INFORMATION:  
APPLICANT: NAKAMURA, No. 6306395io  
APPLICANT: NAGATA, Shigekazu  
TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE  
FILE REFERENCE: 1110-207P

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; CURRENT APPLICATION NUMBER: US/09/180,100
; CURRENT FILING DATE: 1998-11-02
; EARLIER APPLICATION NUMBER: PCT/Jp97/01502
; EARLIER FILING DATE: 1997-05-01
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 335
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-180-100-20

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Query Match 100.0%; Score 557; DB 4; Length 335;  
Best Local Similarity 100.0%; Pred. No. 5e-56;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 11
US-09-565-918-3
; Sequence 3, Application US/09565918
; Patent No. 6433147
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A.
; APPLICANT: Pan, James G.
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Dixit, Vishva M.
; TITLE OF INVENTION: Death Domain Containing Receptor 4
; FILE REFERENCE: 1488.1300005
; CURRENT APPLICATION NUMBER: US/09/565,918
; CURRENT FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: US 60/132,922
; PRIOR FILING DATE: 1999-05-06
; PRIOR APPLICATION NUMBER: US 09/013,895
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: US 60/037,829
; PRIOR FILING DATE: 1997-02-05
; PRIOR APPLICATION NUMBER: US 60/035,722
; PRIOR FILING DATE: 1997-01-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 3
; LENGTH: 335
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-565-918-3

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	Query Match	100.0%;	Score 557;	DB 4;	Length 335;
	Best Local Similarity	100.0%;	Pred. No. 5e-56;		
	Matches 111; Conservative	0;	Mismatches	0;	Gaps
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Dq	218	ETVAINLSDVDLSKYITTTIAGVMTL	SOVGKFVRKNGVN	EAKIDEIKNDNVODTAEQKVQL	277

QY	61	LRNWHQLHGKKEAYDTLIKDKKANLCTLAEKIQTIIKDIITSDSENSFR	111
D <sub>b</sub>	278	LRNWHQLHGKKEAYDTLIKDKKANLCTLAEKIQTIIKDIITSDSENSFR	328

RESULT 12  
US-09-573-986-7  
; Sequence 7, Application US/09573986  
; Patent No. 6455040  
; GENERAL INFORMATION:

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; APPLICANT: Wei, Ying-Fei
; APPLICANT: Ni, Jian
; APPLICANT: Gentz, Reiner
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
; FILE REFERENCE: 1488.1280004
; CURRENT APPLICATION NUMBER: US/09/573,986
; CURRENT FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 335
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-573-986-7

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Query Match	100.0%;	Score 557;	DB 4;	Length 335;
Best Local Similarity	100.0%;	Pred. No. 5e-56;		
Matches 111;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;

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Dd	218	ETVAINLSDDVLDSKYITTTIAGVMWTL	SQVKGFVRKNGVN	EAKIDEIKNDNVQDTAEQKVQL	277
Qy	61	LRNWHQLHGKKEAYDTHLKDILKKANLCT	LAEKIQTIILKDI	TSDSENSNFR	111
Dd	278	LRNWHQLHGKKEAYDTHLKDILKKANLCT	LAEKIQTIILKDI	TSDSENSNFR	328

RESULT 13

US-09-665-615B-2

; Sequence 2, Application US/09665615B

; Patent No. 6653133

; GENERAL INFORMATION:

; APPLICANT: Dean, Nicholas M.

; APPLICANT: Marcusson, Eric G.

; APPLICANT: Wyatt, Jacqueline

; TITLE OF INVENTION: Antisense Modulation of Fas Mediated Signaling

; FILE REFERENCE: ISPH-0502

; CURRENT APPLICATION NUMBER: US/09/665,615B

; CURRENT FILING DATE: 2000-09-18

; PRIOR APPLICATION NUMBER: US 09/290,640

; PRIOR FILING DATE: 1999-04-12

; NUMBER OF SEQ ID NOS: 179

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2

; LENGTH: 335

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-665-615B-2

Query Match	100.0%;	Score 557;	DB 4;	Length 335;
Best Local Similarity	100.0%;	Pred. No. 5e-56;		
Matches 111;	Conservative	0;	Mismatches	0;
			Indels	0;
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[illegible]

RESULT 14  
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; Sequence 2, Application PC/TUS9517083  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: SECRETED HUMAN FAS ANTIGEN  
; NUMBER OF SEQUENCES: 16  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/17083



; FILING DATE: CONCURRENTLY HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/371,263
; FILING DATE: 23-DEC-1994
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 335 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
PCT-US95-17083-2

Query Match 100.0%; Score 557; DB 5; Length 335;
Best Local Similarity 100.0%; Pred. No. 5e-56;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETVAINLSVDLSKYITTTIAGVMTLSQVKGfVRKNGVNEAKIDEIKNDNVQDTAEQKVQL 60
Db 218 ETVAINLSVDLSKYITTTIAGVMTLSQVKGfVRKNGVNEAKIDEIKNDNVQDTAEQKVQL 277

QY 61 LRNWHQLHGKKEAYDTLIKDLKKANLCTLAEKIQTIILKDIITSDSENSNFR 111
Db 278 LRNWHQLHGKKEAYDTLIKDLKKANLCTLAEKIQTIILKDIITSDSENSNFR 328

RESULT 15
US-09-013-895A-3
; Sequence 3, Application US/09013895A
; Patent No. 6342363
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A.
; APPLICANT: Pan, James G.
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Dixit, Vishva M.
; TITLE OF INVENTION: Death Domain Containing Receptor 4 (DR4: Death
; TITLE OF INVENTION: Receptor 4), Member of the TNF-Receptor
; TITLE OF INVENTION: Superfamily and Binding to Trail (AP02-L)
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/013,895A
; FILING DATE: 27-JAN-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.13000002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 669 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-013-895A-3

Query Match 100.0%; Score 557; DB 4; Length 669;
Best Local Similarity 100.0%; Pred. No. 1.2e-55;

Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETVAINLSVDLSKYITTTIAGVMTLSQVKGfVRKNGVNEAKIDEIKNDNVQDTAEQKVQL 60
Db 218 ETVAINLSVDLSKYITTTIAGVMTLSQVKGfVRKNGVNEAKIDEIKNDNVQDTAEQKVQL 277

QY 61 LRNWHQLHGKKEAYDTLIKDLKKANLCTLAEKIQTIILKDIITSDSENSNFR 111
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Job time : 14.9581 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 1, 2004, 14:43:57 ; Search time 35.8922 Seconds  
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Title: US-09-854-906-9  
Perfect score: 557  
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Gapop 10.0 , Gapext 0.5

Searched: 1151071 seqs, 279249464 residues

Total number of hits satisfying chosen parameters: 1151071

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

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- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
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- 18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	557	100.0	335	9	US-09-826-212-7	Sequence 7, Appli
2	557	100.0	335	9	US-09-802-669-2	Sequence 2, Appli
3	557	100.0	335	9	US-09-333-966-6	Sequence 6, Appli
4	557	100.0	335	9	US-09-949-713-20	Sequence 20, Appli
5	557	100.0	335	9	US-09-874-138-4	Sequence 4, Appli
6	557	100.0	335	9	US-09-894-987-2	Sequence 2, Appli
7	557	100.0	335	9	US-09-935-727-9	Sequence 9, Appli
8	557	100.0	335	10	US-09-314-889-6	Sequence 6, Appli
9	557	100.0	335	12	US-10-619-220-2	Sequence 2, Appli
10	557	100.0	335	13	US-10-005-842-4	Sequence 4, Appli
11	557	100.0	335	14	US-10-175-902-3	Sequence 3, Appli
12	557	100.0	335	14	US-10-186-643-7	Sequence 7, Appli
13	557	100.0	335	14	US-10-189-189-6	Sequence 6, Appli
14	557	100.0	335	15	US-10-418-242-9	Sequence 9, Appli
15	557	100.0	669	14	US-10-226-296-3	Sequence 3, Appli

16	557	100.0	669	14	US-10-226-318-3	Sequence 3, Appli
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18	515	92.5	104	15	US-10-359-439-2	Sequence 2, Appli
19	393	70.6	77	12	US-10-207-295-11	Sequence 11, Appli
20	393	70.6	77	13	US-10-112-793-24	Sequence 24, Appli
21	386	69.3	77	9	US-09-887-879-17	Sequence 17, Appli
22	386	69.3	77	9	US-09-992-964-17	Sequence 17, Appli
23	386	69.3	77	14	US-10-242-383-17	Sequence 17, Appli
24	352	63.2	68	9	US-09-756-854-22	Sequence 22, Appli
25	352	63.2	68	13	US-10-041-574-22	Sequence 22, Appli
26	328	58.9	63	13	US-10-035-408-1	Sequence 1, Appli
27	278.5	50.0	327	9	US-09-802-669-66	Sequence 66, Appli
28	278.5	50.0	327	12	US-10-619-220-66	Sequence 66, Appli
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30	237	42.5	281	13	US-10-041-574-3	Sequence 3, Appli
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32	118	21.2	95	12	US-10-218-779-87	Sequence 87, Appli
33	118	21.2	95	12	US-09-972-211-128	Sequence 128, App
34	118	21.2	95	12	US-10-096-625-128	Sequence 128, App
35	118	21.2	96	11	US-09-970-944-45	Sequence 45, Appli
36	118	21.2	96	12	US-10-037-417-124	Sequence 124, App
37	84.5	15.2	83	11	US-09-970-944-47	Sequence 47, Appli
38	84.5	15.2	83	12	US-10-037-417-126	Sequence 126, App
39	84.5	15.2	276	15	US-10-264-213-242	Sequence 242, App
40	83.5	15.0	82	12	US-10-087-684-89	Sequence 89, Appli
41	83.5	15.0	82	12	US-10-218-779-89	Sequence 89, Appli
42	82	14.7	261	15	US-10-264-213-227	Sequence 227, App
43	80.5	14.5	656	9	US-09-862-027-30	Sequence 30, Appli
44	80.5	14.5	1182	12	US-10-282-122A-53445	Sequence 53445, A
45	78.5	14.1	77	14	US-10-287-594-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1  
US-09-826-212-7  
; Sequence 7, Application US/09826212  
; Patent No. US20010021516A1  
; GENERAL INFORMATION:  
; APPLICANT: Wei, Ying-Fei  
; APPLICANT: Gentz, Reiner  
; APPLICANT: Ruben, Steven  
; APPLICANT: Ni, Jian  
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5  
; FILE REFERENCE: 1488.1280006  
; CURRENT APPLICATION NUMBER: US/09/826,212  
; CURRENT FILING DATE: 2001-04-05  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 7  
; LENGTH: 335  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-826-212-7

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Best Local Similarity	100.0%;	Pred. No.	4.1e-51;				
Matches	111;	Conservative	0;	Mismatches	0;	Indels	0;
		Gaps	0;				
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Db	218	ETVAINLSVDLSKYITTTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVQL	277				
QY	61	LRNWHQLHGKKEAYDTLTKDLKCANLCTLAEKIQTIILKDITSDSENSNFR	111				
Db	278	LRNWHQLHGKKEAYDTLTKDLKCANLCTLAEKIQTIILKDITSDSENSNFR	328				

RESULT 2  
US-09-802-669-2  
; Sequence 2, Application US/09802669  
; Patent No. US20020004490A1

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; GENERAL INFORMATION:
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Marcusson, Eric G.
; APPLICANT: Wyatt, Jacqueline
; APPLICANT: Zhang, Hong
; TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
; FILE REFERENCE: ISPH-545
; CURRENT APPLICATION NUMBER: US/09/802,669
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: US 09/665,615
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 09/290,640
; PRIOR FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 335
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-802-669-2

Query Match          100.0%; Score 557; DB 9; Length 335;
Best Local Similarity 100.0%; Pred. No. 4.1e-51;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
US-09-333-966-6
; Sequence 6, Application US/09333966
; Patent No. US20020009773A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ni, Jian
; APPLICANT: Dixit, Vishva
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Dillon, Patrick J.
; TITLE OF INVENTION: Death Domain Containing Receptors
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., NW, Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/333,966
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/815,469
; FILING DATE:
; APPLICATION NUMBER: No. US20020009773A1 Yet Assigned
; FILING DATE: 06-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/028,711
; FILING DATE: 17-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,285
; FILING DATE: 12-MAR-1996

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; ATTORNEY/AGENT INFORMATION:
; NAME: Steffe, Eric K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 335 amino acids
; TYPE: amino acid
; STRANDEDNESS: No. US20020009773A1 Relevant
; TOPOLOGY: No. US20020009773A1 Relevant
; MOLECULE TYPE: protein
US-09-333-966-6

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Best Local Similarity 100.0%; Pred. No. 4.1e-51;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      61  LRNWHQLHGKKEAYDTLTKDLKKANLCTLAEKIQTIILKDIITSDSENSNFR 111
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RESULT 4
US-09-949-713-20
; Sequence 20, Application US/09949713
; Patent No. US20020044944A1
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, No. US20020044944A1io
; APPLICANT: NAGATA, Shigekazu
; TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE
; FILE REFERENCE: 1110-207P
; CURRENT APPLICATION NUMBER: US/09/949,713
; CURRENT FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US/09/180,100
; PRIOR FILING DATE: 1998-11-02
; PRIOR APPLICATION NUMBER: PCT/JP97/01502
; PRIOR FILING DATE: 1997-05-01
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
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; LENGTH: 335
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-949-713-20

Query Match          100.0%; Score 557; DB 9; Length 335;
Best Local Similarity 100.0%; Pred. No. 4.1e-51;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      61  LRNWHQLHGKKEAYDTLTKDLKKANLCTLAEKIQTIILKDIITSDSENSNFR 111
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Db      278 LRNWHQLHGKKEAYDTLTKDLKKANLCTLAEKIQTIILKDIITSDSENSNFR 328

RESULT 5
US-09-874-138-4
; Sequence 4, Application US/09874138
; Patent No. US20020072091A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Yu, Guo-liang

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; APPLICANT: Rosen, Craig A.  
; TITLE OF INVENTION: Death Domain Containing Receptor 5  
; FILE REFERENCE: 1488.1310006  
; CURRENT APPLICATION NUMBER: US/09/874,138  
; CURRENT FILING DATE: 2001-06-06  
; PRIOR APPLICATION NUMBER: 09/565,009  
; PRIOR FILING DATE: 2000-05-04  
; PRIOR APPLICATION NUMBER: 60/148,939  
; PRIOR FILING DATE: 1999-08-13  
; PRIOR APPLICATION NUMBER: 60/133,238  
; PRIOR FILING DATE: 1999-05-07  
; PRIOR APPLICATION NUMBER: 60/132,498  
; PRIOR FILING DATE: 1999-05-04  
; PRIOR APPLICATION NUMBER: 09/042,583  
; PRIOR FILING DATE: 1998-03-17  
; PRIOR APPLICATION NUMBER: 60/054,021  
; PRIOR FILING DATE: 1997-07-29  
; PRIOR APPLICATION NUMBER: 60/040,846  
; PRIOR FILING DATE: 1997-03-17  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 335  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-874-138-4

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Best Local Similarity 100.0%; Pred. No. 4.1e-51;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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QY 61 LRNWHQLHGKKEAYDTLIKDLKKANLCTLAEKIQTIILKDITSDSENSNFR 111  
Db 278 LRNWHQLHGKKEAYDTLIKDLKKANLCTLAEKIQTIILKDITSDSENSNFR 328

RESULT 6  
US-09-884-987-2  
; Sequence 2, Application US/09884987  
; Patent No. US20020102653A1  
; GENERAL INFORMATION:  
; APPLICANT: NAGATA, Shigekazu et al  
; TITLE OF INVENTION: DNA CODING FOR HUMAN CELL SURFACE ANTIGEN  
; FILE REFERENCE: 0020-4877P  
; CURRENT APPLICATION NUMBER: US/09/884,987  
; CURRENT FILING DATE: 2001-06-21  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2  
; LENGTH: 335  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-884-987-2

Query Match 100.0%; Score 557; DB 9; Length 335;  
Best Local Similarity 100.0%; Pred. No. 4.1e-51;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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QY 61 LRNWHQLHGKKEAYDTLIKDLKKANLCTLAEKIQTIILKDITSDSENSNFR 111  
Db 278 LRNWHQLHGKKEAYDTLIKDLKKANLCTLAEKIQTIILKDITSDSENSNFR 328

RESULT 7  
US-09-935-727-9

; Sequence 9, Application US/09935727  
; Patent No. US20020150583A1  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta  
; FILE REFERENCE: PF454P2  
; CURRENT APPLICATION NUMBER: US/09/935,727  
; CURRENT FILING DATE: 2001-08-24  
; PRIOR APPLICATION NUMBER: 60/303,224  
; PRIOR FILING DATE: 2001-07-06  
; PRIOR APPLICATION NUMBER: 60/252,131  
; PRIOR FILING DATE: 2000-11-21  
; PRIOR APPLICATION NUMBER: 60/227,598  
; PRIOR FILING DATE: 2000-08-25  
; PRIOR APPLICATION NUMBER: 09/518,931  
; PRIOR FILING DATE: 2000-03-03  
; PRIOR APPLICATION NUMBER: 60/168,235  
; PRIOR FILING DATE: 1999-12-01  
; PRIOR APPLICATION NUMBER: 60/146,371  
; PRIOR FILING DATE: 1999-08-02  
; PRIOR APPLICATION NUMBER: 60/131,964  
; PRIOR FILING DATE: 1999-04-30  
; PRIOR APPLICATION NUMBER: 60/131,270  
; PRIOR FILING DATE: 1999-04-27  
; PRIOR APPLICATION NUMBER: 60/124,092  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/121,774  
; PRIOR FILING DATE: 1999-03-04  
; PRIOR APPLICATION NUMBER: 09/006,352  
; PRIOR FILING DATE: 1998-01-13  
; PRIOR APPLICATION NUMBER: 60/035,496  
; PRIOR FILING DATE: 1997-01-14  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 9  
; LENGTH: 335  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-935-727-9

Query Match 100.0%; Score 557; DB 9; Length 335;  
Best Local Similarity 100.0%; Pred. No. 4.1e-51;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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Db 218 ETVAINLSDVDSLKYITTIAGVMTLSQVKGfVRKNGVNEAKIDEIKNDNVQDTAEQKVQL 277  
  
QY 61 LRNWHQLHGKKEAYDTLIKDLKKANLCTLAEKIQTIILKDITSDSENSNFR 111  
Db 278 LRNWHQLHGKKEAYDTLIKDLKKANLCTLAEKIQTIILKDITSDSENSNFR 328

RESULT 8  
US-09-314-889-6  
; Sequence 6, Application US/09314889  
; Publication No. US20030077694A1  
; GENERAL INFORMATION:  
; APPLICANT: Yu, Guo-Liang  
; APPLICANT: Ni, Jian  
; APPLICANT: Dixit, Vishva  
; APPLICANT: Gentz, Reiner L.  
; APPLICANT: Dillon, Patrick J.  
; TITLE OF INVENTION: Death Domain Containing Receptors  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.  
; STREET: 1100 New York Ave., NW, Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:



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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible.
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/09/314,889
  FILING DATE:
  CLASSIFICATION:
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: 08/815,469
    FILING DATE:
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 60/028,711
    FILING DATE: 17-OCT-1996
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 60/013,285
    FILING DATE: 12-MAR-1996
  ATTORNEY/AGENT INFORMATION:
    NAME: Steffe, Eric K.
    REGISTRATION NUMBER: 36,688
    REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM
  TELEPHONE: 202-371-2600
  TELEFAX: 202-371-2540
  INFORMATION FOR SEQ ID NO: 6:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 335 amino acids
      TYPE: amino acid
      STRANDEDNESS: not relevant
      TOPOLOGY: not relevant
      MOLECULE TYPE: protein
US-09-314-889-6

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Query Match      100.0%; Score 557; DB 10; Length 335;
Best Local Similarity 100.0%; Pred. No. 4.1e-51;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

y      1  ETVAINLSDVDLSKYITTTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVQL 60
      |||
b      218 ETVAINLSDVDLSKYITTTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVQL 277

y      61  LRNWHQLHGKGEAYDTLLKDLKKANLCTLAEKIQTIILKDITSDSENSFR 111
      |||
b      278 LRNWHQLHGKGEAYDTLLKDLKKANLCTLAEKIQTIILKDITSDSENSFR 328

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RESULT 9  
US-10-619-220-2  
; Sequence 2, Application US/10619220  
; Publication No. US20040033979A1  
; GENERAL INFORMATION:  
; APPLICANT: Dean, Nicholas M.  
; APPLICANT: Marcusson, Eric G.  
; APPLICANT: Wyatt, Jacqueline  
; APPLICANT: Zhang, Hong  
; TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling  
; FILE REFERENCE: ISPH-545  
; CURRENT APPLICATION NUMBER: US/10/619,220  
; CURRENT FILING DATE: 2003-07-14  
; PRIOR APPLICATION NUMBER: 09/802,669  
; PRIOR FILING DATE: 2001-03-01  
; PRIOR APPLICATION NUMBER: US 09/665,615  
; PRIOR FILING DATE: 2000-09-18  
; PRIOR APPLICATION NUMBER: US 09/290,640  
; PRIOR FILING DATE: 1999-04-12  
; NUMBER OF SEQ ID NOS: 180  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 335  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-619-220-2

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	Best Local Similarity	100.0%;	Pred. No. 4.1e-51;		
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Dd	218	ETVAINLSVDLSKYITTIAGVMTLSQVKGFVRKNGVNEAKIDEIKNDNVQDTAEQKVQL	277		
QY	61	LRNWHLGKKKEYDTLIKDKKANLCTLAEKIQTIILKDITSSENSFR	111		
Dd	278	LRNWHLGKKKEYDTLIKDKKANLCTLAEKIQTIILKDITSSENSFR	328		

RESULT 10  
US-10-005-842-4  
; Sequence 4, Application US/10005842  
; Publication No. US20020098550A1  
; GENERAL INFORMATION:  
; APPLICANT: Ni, Jian  
;     Gentz, Reiner  
;     Yu, Guo-Liang  
;     Su, Jeffrey  
;     Rosen, Craig A.  
; TITLE OF INVENTION: Death Domain Containing Receptor 5  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
;     ADDRESSEE: Human Genome Sciences, Inc.  
;     STREET: 9410 Key West Avenue  
;     CITY: Rockville  
;     STATE: MD  
;     COUNTRY: US  
;     ZIP: 20850  
; COMPUTER READABLE FORM:  
;     MEDIUM TYPE: Floppy disk  
;     COMPUTER: IBM PC compatible  
;     OPERATING SYSTEM: PC-DOS/MS-DOS  
;     SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
;     APPLICATION NUMBER: US/10/005,842  
;     FILING DATE: 07-Dec-2001  
;     CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
;     APPLICATION NUMBER: 09/042,583  
;     FILING DATE: <Unknown>  
;     APPLICATION NUMBER: US 60/040,846  
;     FILING DATE: 17-MAR-1997  
; ATTORNEY/AGENT INFORMATION:  
;     NAME: Hoover, Kenley  
;     REGISTRATION NUMBER: 40,302  
;     REFERENCE/DOCKET NUMBER: PF366  
; TELECOMMUNICATION INFORMATION:  
;     TELEPHONE: 3013098504  
;     TELEFAX: 3013098439  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
;     LENGTH: 335 amino acids  
;     TYPE: amino acid  
;     STRANDEDNESS: single  
;     TOPOLOGY: linear  
;     MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-10-005-842-4

	Query Match	100.0%;	Score 557;	DB 13;	Length 335;
	Best Local Similarity	100.0%;	Pred. No. 4.1e-51;		
	Matches 111;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0
QY	1	ETVAINLSDVDLSKYITTIAGVMTLSQVKGFVRKNGVNEAKIDEIKNDNVQDTAEQKVQL	60		
Db	218	ETVAINLSDVDLSKYITTIAGVMTLSQVKGFVRKNGVNEAKIDEIKNDNVQDTAEQKVQL	277		
QY	61	LRNWHQLHGKKEAYDTLIKDLKKANLCTLAEKIQTIILKIDITSSENSNFR	111		



; CURRENT FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: 60/373,604
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 09/935,727
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/303,224
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: 60/252,131
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: 60/227,598
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: 09/518,931
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/168,235
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 60/146,371
; PRIOR FILING DATE: 1999-08-02
; PRIOR APPLICATION NUMBER: 60/131,964
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: 60/131,279
; PRIOR FILING DATE: 1999-04-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 51
; SEQ ID NO 9
; LENGTH: 335
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-418-242-9

Query Match 100.0%; Score 557; DB 15; Length 335;
Best Local Similarity 100.0%; Pred. No. 4.1e-51;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETVAINLSDVDLSKYITTTIAGVMTLSQVKGFVRKNGVNEAKIDEIKNDNVQDTAEQKVQL 60
Db ETVAINLSDVDLSKYITTTIAGVMTLSQVKGFVRKNGVNEAKIDEIKNDNVQDTAEQKVQL 277

QY 61 LRNWHQLHGKKEAYDTLLKDLKANLCTLAEKIQTIILKDITSDSENSNFR 111
Db LRNWHQLHGKKEAYDTLLKDLKANLCTLAEKIQTIILKDITSDSENSNFR 328

RESULT 15
US-10-226-296-3
; Sequence 3, Application US/10226296
; Publication No. US20030036168A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; Rosen, Craig A.
; Pan, James G.
; Gentz, Reiner L.
; Dixit, Vishva M.
; TITLE OF INVENTION: Death Domain Containing Receptor 4 (DR4: Death
; Receptor 4), Member of the TNF-Receptor
; Superfamily and Binding to Trail (AP02-L)
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/226,296
; FILING DATE: 23-Aug-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/09/448,868
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 09/013,895
; FILING DATE: 27-JAN-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.1300004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202)371-2540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 669 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-226-296-3

Query Match 100.0%; Score 557; DB 14; Length 669;
Best Local Similarity 100.0%; Pred. No. 1e-50;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETVAINLSDVDLSKYITTTIAGVMTLSQVKGFVRKNGVNEAKIDEIKNDNVQDTAEQKVQL 60
Db ETVAINLSDVDLSKYITTTIAGVMTLSQVKGFVRKNGVNEAKIDEIKNDNVQDTAEQKVQL 277

QY 61 LRNWHQLHGKKEAYDTLLKDLKANLCTLAEKIQTIILKDITSDSENSNFR 111
Db LRNWHQLHGKKEAYDTLLKDLKANLCTLAEKIQTIILKDITSDSENSNFR 328

Search completed: June 1, 2004, 14:50:04
Job time : 35.8922 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 1, 2004, 14:37:07 ; Search time 11.6317 Seconds  
(without alignments)  
917.942 Million cell updates/sec

Title: US-09-854-906-9  
Perfect score: 557  
Sequence: 1 ETVAINLSVDLSKYITIA.....KIQTIIILKDITSDSENSNFR 111

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_78:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	557	100.0	314	2 I37383	FAS soluble protei
2	557	100.0	335	2 A40036	apoptosis-mediati
3	278.5	50.0	327	2 A46484	apoptosis-mediati
4	250.5	45.0	324	2 JC2395	Fas antigen precu
5	86.5	15.5	1979	2 C71622	hypothetical prote
6	81.5	14.6	589	2 C97241	methyl-accepting c
7	80.5	14.5	656	2 I49299	receptor interacti
8	78.5	14.1	671	2 T09479	serine/threonine p
9	78.5	14.1	4196	2 T43274	dynein heavy chain
10	77.5	13.9	416	2 A45105	farnesyl-diphospha
11	77.5	13.9	1558	2 B71603	RESA-H3 antigen PF
12	76.5	13.7	275	2 S40903	FUN4 protein - yea
13	76	13.6	406	2 I39932	replication protei
14	76	13.6	640	2 AE1895	hypothetical prote
15	75.5	13.6	265	2 I41162	DNA-binding protei
16	75	13.5	261	2 S14875	dnaK-type molecula
17	75	13.5	265	2 A31457	xns protein - Esch
18	75	13.5	671	2 D72346	chemotaxis sensor
19	74	13.3	106	2 D86641	transcription regu
20	74	13.3	191	2 H71045	hypothetical prote
21	74	13.3	548	2 G97047	single-stranded-DN
22	74	13.3	575	2 S46692	hypothetical prote
23	73.5	13.2	365	2 C70116	recombination prot
24	73.5	13.2	395	2 T50804	hypothetical prote
25	73.5	13.2	643	2 B71848	probable outer mem
26	73	13.1	227	2 G70182	hypothetical prote
27	73	13.1	371	2 T21819	hypothetical prote
28	73	13.1	461	2 JC4302	tumor necrosis fac
29	73	13.1	552	2 T04653	receiver-like prot

30	73	13.1	657	2 A53545	protein p84 - huma
31	73	13.1	1169	2 A64505	Pil5 homolog - Met
32	72.5	13.0	386	2 B71407	hypothetical prote
33	72.5	13.0	512	2 F90124	t-complex proteini
34	72.5	13.0	778	2 JC7797	scallop unconventi
35	72	12.9	458	2 S75328	DNA-directed DNA p
36	72	12.9	1176	1 A48047	phospholipase C (E
37	72	12.9	1195	2 A59016	DNA-directed DNA p
38	72	12.9	1830	2 E82909	conserved hypothet
39	71.5	12.8	297	2 E90518	DNA polymerase III
40	71.5	12.8	320	2 A81434	molybdenum cofacto
41	71.5	12.8	326	2 G95235	conserved hypothet
42	71.5	12.8	326	2 H98099	conserved hypothet
43	71.5	12.8	555	2 F83982	hypothetical prote
44	71.5	12.8	1039	2 S62509	probable vesicular
45	71.5	12.8	1044	2 T50213	probable vesicular

ALIGNMENTS

RESULT 1

I37383  
FAS soluble protein - human  
C;Species: Homo sapiens (man)  
C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 07-Jul-2003  
C;Accession: I37383  
R;Cascino, I.; Fiucci, G.; Papoff, G.; Ruberti, G.  
J. Immunol. 154, 2706-2713, 1995  
A;Title: Three functional soluble forms of the human apoptosis-inducing Fas molecule are  
A;Reference number: I37383; MUID:95181785; PMID:7533181  
A;Accession: I37383  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: mRNA  
A;Residues: 1-314 <RES>  
A;Cross-references: EMBL:Z47993; NID:g728578; PIDN:CAA88031.1; PID:g695539  
C;Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology

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Best Local Similarity 100.0%; Pred. No. 7.1e-41;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ETVAINLSVDLSKYITTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVQL	60
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QY	61	LRNWHQHGKKEAYDTLIKDLKANLCTLAETIILKDITSDSENSNFR	111
Db	257	LRNWHQHGKKEAYDTLIKDLKANLCTLAETIILKDITSDSENSNFR	307

RESULT 2

A40036  
apoptosis-mediating surface antigen Fas precursor - human  
N;Alternate names: surface antigen APO-1  
C;Species: Homo sapiens (man)  
C;Date: 17-Jan-1992 #sequence\_revision 17-Jan-1992 #text\_change 07-Jul-2003  
C;Accession: A40036; S24543; A38142  
R;Itoh, N.; Yonehara, S.; Ishii, A.; Yonehara, M.; Mizushima, S.I.; Sameshima, M.; Hase, Cell 66, 233-243, 1991  
A;Title: The polypeptide encoded by the cDNA for human cell surface antigen Fas can medi  
A;Reference number: A40036; MUID:91309137; PMID:1713127  
A;Accession: A40036  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-335 <ITO>  
A;Cross-references: GB:M67454; NID:g182409; PIDN:AAA63174.1; PID:g182410  
R;Krammer, P.H.  
submitted to the EMBL Data Library, February 1992  
A;Reference number: S24543  
A;Accession: S24543  
A;Status: preliminary  
A;Molecule type: mRNA



A;Residues: 1-335 <KRA>  
A;Cross-references: EMBL:X63717; NID:g28741; PID:g28742  
R;Oehm, A.; Behrmann, I.; Falk, W.; Pawlita, M.; Maier, G.; Klas, C.; Li-Weber, M.; Rich  
J. Biol. Chem. 267, 10709-10715, 1992  
A;Title: Purification and molecular cloning of the APO-1 cell surface antigen, a member  
A;Reference number: A38142; MUID:92268122; PMID:1375228  
A;Accession: A38142  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: nucleic acid  
A;Residues: 1-134,'Q',136-335 <OEH>  
A;Experimental source: SKW6.4 cells  
A;Note: sequence extracted from NCBI backbone (NCBIP:103810)  
A;Note: in NCBI backbone the source is designated as mouse  
C;Genetics:  
A;Gene: GDB:APT1  
A;Cross-references: GDB:132671; OMIM:134637  
A;Map position: 10q24.1-10q24.1  
C;Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology  
C;Keywords: apoptosis; surface antigen; transmembrane protein  
F;1-16/Domain: signal sequence #status predicted <SIG>  
F;85-128/Domain: NGF receptor repeat homology <NG4>  
F;174-190/Domain: transmembrane #status predicted <TMM>  
  
Query Match 100.0%; Score 557; DB 2; Length 335;  
Best Local Similarity 100.0%; Pred. No. 7.6e-41;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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Db |||||  
218 ETVAINLSDVLSKYITTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVQL 277  
  
QY 61 LRNWHQLHGKKEAYDTLTKLKKANLCTLAEKIQTIILKDITSDSENSNFR 111  
Db |||||  
278 LRNWHQLHGKKEAYDTLTKLKKANLCTLAEKIQTIILKDITSDSENSNFR 328  
  
RESULT 3  
A46484  
apoptosis-mediating membrane-associated polypeptide Fas - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 18-Jun-1993 #sequence\_revision 18-Nov-1994 #text\_change 07-Jul-2003  
C;Accession: A46484; A47254  
R;Watanabe-Fukunaga, R.; Brannan, C.I.; Itoh, N.; Yonehara, S.; Copeland, N.G.; Jenkins,  
J. Immunol. 148, 1274-1279, 1992  
A;Title: The cDNA structure, expression, and chromosomal assignment of the mouse Fas and  
A;Reference number: A46484; MUID:92148151; PMID:1371136  
A;Accession: A46484  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-327 <WAT>  
A;Cross-references: GB:M83649; NID:g193225; PIDN:AAA37593.1; PID:g193226  
A;Experimental source: B6M3 macrophage cell line  
A;Note: sequence extracted from NCBI backbone (NCBIN:81544, NCBIP:81545)  
R;Adachi, M.; Watanabe-Fukunaga, R.; Nagata, S.  
Proc. Natl. Acad. Sci. U.S.A. 90, 1756-1760, 1993  
A;Title: Aberrant transcription caused by the insertion of an early transposable element  
A;Reference number: A47254; MUID:93189576; PMID:7680478  
A;Accession: A47254  
A;Status: preliminary  
A;Molecule type: nucleic acid  
A;Residues: 1-96 <ADA>  
A;Cross-references: GB:S56490; NID:g298505; PIDN:AAB25700.1; PID:g298506  
A;Experimental source: MRL lpr/lpr  
A;Note: sequence extracted from NCBI backbone (NCBIN:126850, NCBIN:126853, NCBIN:126863,  
C;Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology  
C;Keywords: transmembrane protein  
F;44-79/Domain: NGF receptor repeat homology <NGF>  
F;81-124/Domain: NGF receptor repeat homology <NG4>  
  
Query Match 50.0%; Score 278.5; DB 2; Length 327;  
Best Local Similarity 50.9%; Pred. No. 8.5e-17;  
Matches 57; Conservative 18; Mismatches 34; Indels 3; Gaps 1;

QY 1 ETVAINLSDVLSKYITTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVQL 60  
Db |||||  
210 ETIPMNASNLSSKYIPRIAEEDMTIQEAKKFARENNIKEGKIDEIMHDSIQDTAEQKVQL 269  
  
QY 61 LRNWHQLHGKKEAYDTLTKLKKANLCTLAEKIQTIILKDI---TSDSENSN 109  
Db |||||  
270 LLCWYQSHGKSDAYQDLIKGLKKAECRRTLDFQDMVQKOLGKSTPDTGNEN 321  
  
RESULT 4  
JC2395  
Fas antigen precursor - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 07-Jul-2003  
C;Accession: JC2395; PC2246  
R;Kimura, K.; Wakatsuki, T.; Yamamoto, M.  
Biochem. Biophys. Res. Commun. 198, 666-674, 1994  
A;Title: A variant mRNA species encoding a truncated form of Fas antigen in the rat liv  
A;Reference number: JC2395; MUID:94128114; PMID:7507668  
A;Accession: JC2395  
A;Molecule type: mRNA  
A;Residues: 1-324 <KIM>  
A;Cross-references: DDBJ:D26112; NID:g468486; PIDN:BAA05108.1; PID:d1005650; PID:g46848  
A;Experimental source: thymus  
A;Accession: PC2246  
A;Molecule type: mRNA  
A;Residues: 1-62,'RFT', <KI2>  
A;Cross-references: DDBJ:D26113; NID:g468488; PIDN:BAA05109.1; PID:d1005651; PID:g46848  
A;Experimental source: liver  
C;Genetics:  
A;Introns: 62/1  
C;Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology  
C;Keywords: transmembrane protein  
F;1-21/Domain: signal sequence #status predicted <SIG>  
F;22-324/Product: Fas antigen #status predicted <MAT>  
F;44-79/Domain: NGF receptor repeat homology <NGF>  
F;81-124/Domain: NGF receptor repeat homology <NG4>  
F;171-188/Domain: transmembrane #status predicted <TMM>  
  
Query Match 45.0%; Score 250.5; DB 2; Length 324;  
Best Local Similarity 46.4%; Pred. No. 2.2e-14;  
Matches 52; Conservative 25; Mismatches 32; Indels 3; Gaps 1;  
  
QY 1 ETVAINLSDVLSKYITTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVQL 60  
Db |||||  
207 ESVPNVSDVNLNKYIWRTAEKWKICDAKKFARQHKIPESKIDEIHNSPQDAAEQKIQL 266  
  
QY 61 LRNWHQLHGKKEAYDTLTKLKKANLCTLAEKIQTIILKD---ITSDSENSN 109  
Db |||||  
267 LQCWYQSHGKTGACQALIQGLRKRANRCDIAEEIQAMVWEDHENSISNRNEN 318  
  
RESULT 5  
C71622  
hypothetical protein PFB0145c - malaria parasite (Plasmodium falciparum)  
C;Species: Plasmodium falciparum  
C;Date: 13-Nov-1998 #sequence\_revision 13-Nov-1998 #text\_change 21-Jul-2000  
C;Accession: C71622  
R;Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.  
.; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O  
Science 282, 1126-1132, 1998  
A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.  
A;Reference number: A71600; MUID:99021743; PMID:9804551  
A;Accession: C71622  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-1979 <GAR>  
A;Cross-references: GB:AB001375; GB:AB001362; NID:g3845105; PIDN:AAC71819.1; PID:g38451  
A;Experimental source: clone 3D7  
C;Genetics:  
A;Gene: PFB0145c  
  
Query Match 15.5%; Score 86.5; DB 2; Length 1979;





Db 251 ISDMKTDKYIATIKGIKKVVSQGMKSFSDIENVEQAYLEERKQLQ-KPKSQQKPNSLK- 308

QY 64 WHQLHGKKEAYDTLLKDLKKANLCTLAEKIQTIILKDTSDSEN 107

Db 309 --PSYGKKDIVPEWLKEQKLKD-----EEVQT--NKLHQNSES 343

RESULT 14  
AE1895  
hypothetical protein all0711 [imported] - Nostoc sp. (strain PCC 7120)  
C;Species: Nostoc sp. PCC 7120  
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
C;Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Dec-2002  
C;Accession: AE1895  
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi  
Nakazaki, N.; Shimpō, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S  
DNA Res. 8, 205-213, 2001  
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana  
A;Reference number: AB1807; MUID:21595285; PMID:11759840  
A;Accession: AE1895  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-640 <KUR>  
A;Cross-references: GB:BA000019; PIDN:BAB72668.1; PID:g17130056; GSPDB:GN00179  
A;Experimental source: strain PCC 7120  
C;Genetics:  
A;Gene: all0711

Query Match 13.6%; Score 76; DB 2; Length 640;  
Best Local Similarity 26.8%; Pred. No. 55;  
Matches 22; Conservative 18; Mismatches 36; Indels 6; Gaps 2;

QY 17 TTIAGVMTLSQVKGFRKGVNEAKIDEIKNDNVQDTAEQKVQLLRNWHQHLHGKKEAYDT 76

Db 562 TVKEAINTNVNIPSWIRSSFVNDRKIDDICK-QVNPELEKVIQ-----EQLTANQDAFDK 615

QY 77 LIKDLKKANLCTLAEKIQTIIL 98

Db 616 LISKVEGLQKALSTKVQEAI 637

RESULT 15  
I41162  
DNA-binding protein cafd - Escherichia coli  
C;Species: Escherichia coli  
C;Date: 31-May-1996 #sequence\_revision 31-May-1996 #text\_change 26-Aug-1999  
C;Accession: I41162  
R;Savelkoul, P.H.; Willshaw, G.A.; McConnell, M.M.; Smith, H.R.; Hamers, A.M.; van der Z  
Microb. Pathog. 8, 91-99, 1990  
A;Title: Expression of CFA/I fimbriae is positively regulated.  
A;Reference number: I41162; MUID:90271755; PMID:1971911  
A;Accession: I41162  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-265 <RES>  
A;Cross-references: GB:M55609; NID:g145505; PIDN:AAA62773.1; PID:g145506  
C;Genetics:  
A;Gene: cfaD  
C;Superfamily: fapR protein

Query Match 13.6%; Score 75.5; DB 2; Length 265;  
Best Local Similarity 23.4%; Pred. No. 23;  
Matches 25; Conservative 22; Mismatches 31; Indels 29; Gaps 3;

QY 29 KGFVRK--NGVNEAKIDEIKNDNVQDTAEQKVQLLRNWHQHLHGKKEAYDTLLKDLKKAN 85

Db 103 RGMSPKIMTTEVNTLLDELKNINSHDDSAFISSLI----YLISKIENNEKIIESIYISS 158

QY 86 LCTLAEKIQTIILKDITS-----DSENSNF 110

Db 159 VSFFSDKVRNVIEKDLRSKWTGLIADAFNVSEITIRKRLESENTNF 205



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 1, 2004, 14:33:56 ; Search time 7.97605 Seconds  
(without alignments)  
724.643 Million cell updates/sec

Title: US-09-854-906-9  
Perfect score: 557  
Sequence: 1 ETVAINLSVDVLSKYITIA.....KIQTIIILKDITSDSENSNR 111

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues  
Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	557	100.0	335	1 TNR6 HUMAN	P25445 homo sapien
2	337	60.5	332	1 TNR6_PIG	O77736 sus scrofa
3	331	59.4	323	1 TNR6_BOVIN	P51867 bos taurus
4	278.5	50.0	327	1 TNR6_MOUSE	P25446 mus musculus
5	250.5	45.0	324	1 TNR6_RAT	Q63199 rattus norv
6	81	14.5	657	1 THOI_MOUSE	Q8r3n6 mus musculus
7	80.5	14.5	656	1 RIKI_MOUSE	Q60855 mus musculus
8	78.5	14.1	343	1 THOI_RAT	P59924 rattus norv
9	78.5	14.1	671	1 RIKI_HUMAN	Q13546 homo sapien
10	78.5	14.1	4196	1 DYHC_SCHPO	O13290 schizosacch
11	77.5	13.9	416	1 FDFT_RAT	Q02769 rattus norv
12	76.5	13.7	275	1 SE34_YEAST	P39707 saccharomyc
13	75.5	13.6	265	1 CFAD_ECOLI	P25393 escherichia
14	75	13.5	265	1 RNS_ECOLI	P16114 escherichia
15	75	13.5	671	1 CHEA_THEMEA	Q56310 thermotoga
16	74	13.3	575	1 YH26_YEAST	P38882 saccharomyc
17	74	13.3	743	1 FTSK_CLOTE	Q895i8 clostridium
18	73.5	13.2	365	1 RECA_BORBU	Q59180 borrelia bu
19	73	13.1	461	1 TRIA_PIG	P50555 sus scrofa
20	73	13.1	471	1 TRIA_BOVIN	O19131 bos taurus
21	73	13.1	508	1 KLC_DROME	P46824 drosophila
22	73	13.1	552	1 ARRA_ARATH	O49397 arabidopsis
23	73	13.1	657	1 THOI_HUMAN	Q96fv9 homo sapien
24	73	13.1	1169	1 SMC_METJA	Q59037 methanococc
25	73	13.1	1175	1 PIB4_HUMAN	Q15147 homo sapien
26	72	12.9	700	1 V018_FOWPV	Q9J5i3 fowlpox vir
27	72	12.9	879	1 RA50_SULTO	Q96yr5 sulfolobus
28	72	12.9	1175	1 PIB4_RAT	Q9qw07 rattus norv
29	72	12.9	1355	1 DP3A_SYNY3	P74750 synecocyst
30	71.5	12.8	320	1 MOAA_CAMJE	Q9piw6 campylobact
31	71.5	12.8	1044	1 YAF3_SCHPO	Q09857 schizosacch
32	71.5	12.8	1075	1 Y124_METJA	Q57588 methanococc
33	71	12.7	205	1 FADD_MOUSE	Q61160 mus musculus

34	70.5	12.7	309	1 EFTS_RICCN	Q92jff4 rickettsia
35	70.5	12.7	530	1 SYK_METJA	Q57959 methanococc
36	70.5	12.7	699	1 HS82_ARATH	P55737 arabidopsis
37	70.5	12.7	699	1 HS83_ARATH	P51818 arabidopsis
38	70.5	12.7	861	1 CHL1_YEAST	P22516 saccharomyc
39	70.5	12.7	992	1 AN18_HUMAN	Q8ivf6 homo sapien
40	70	12.6	156	1 SSB2_STAAM	Q931k4 staphylococ
41	70	12.6	156	1 SSB_STAAN	Q998q9 staphylococ
42	70	12.6	274	1 TRY5_ANOGA	P35039 anopheles g
43	70	12.6	3214	1 BPA1_HUMAN	Q03001 homo sapien
44	69.5	12.5	226	1 RNC_WIGBR	Q8d305 wiggleswort
45	69.5	12.5	404	1 Y452_PYRAB	Q9v1h5 pyrococcus

ALIGNMENTS

RESULT 1  
TNR6\_HUMAN  
ID TNR6\_HUMAN STANDARD; PRT; 335 AA.  
AC P25445; Q14292; Q14293; Q14294; Q14295; Q16652;  
DT 01-MAY-1992 (Rel. 22, Created)  
DT 01-MAY-1992 (Rel. 22, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Tumor necrosis factor receptor superfamily member 6 precursor (FASL receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen) (CD95).  
DE (CD95).  
GN TNFRSF6 OR APT1 OR FAS OR FASL.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RX MEDLINE=91309137; PubMed=1713127;  
RA Itoh N., Yonehara S., Ishii A., Yonehara M., Mizushima S.I.,  
RA Sameshima M., Hase A., Seto Y., Nagata S.;  
RT "The polypeptide encoded by the cDNA for human cell surface antigen Fas can mediate apoptosis.";  
RL Cell 66:233-243(1991).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORM 1), AND SEQUENCE OF 226-240; 269-291 AND 321-335.  
RX MEDLINE=92268122; PubMed=13752228;  
RA Oehm A., Behrmann I., Falk W., Pawlita M., Maier G., Klas C.,  
RA Li-weber M., Richards S., Dhein J., Trauth B.C., Ponstingl H.,  
RA Krammer P.H.;  
RT "Purification and molecular cloning of the APO-1 cell surface antigen, a member of the tumor necrosis factor/nerve growth factor receptor superfamily. Sequence identity with the Fas antigen.";  
RL J. Biol. Chem. 267:10709-10715(1992).  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3 AND 6), AND FUNCTION.  
RX MEDLINE=95181785; PubMed=7533181;  
RA Cascino I., Fiucci G., Papoff G., Ruberti G.;  
RT "Three functional soluble forms of the human apoptosis-inducing Fas molecule are produced by alternative splicing.";  
RL J. Immunol. 154:2706-2713(1995).  
RN [4]  
RP SEQUENCE FROM N.A. (ISOFORM 5).  
RC TISSUE=Peripheral blood lymphocytes;  
RA Schaeetzlein C.E., Poehlmann R., Philippssen P., Eibel H.;  
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE FROM N.A. (ISOFORMS 4 AND 5).  
RX MEDLINE=96238926; PubMed=8648105;  
RA Papoff G., Cascino I., Eramo A., Starace G., Lynch D.H., Ruberti G.;  
RT "An N-terminal domain shared by Fas/Apo-1 (CD95) soluble variants prevents cell death in vitro.";  
RL J. Immunol. 156:4622-4630(1996).  
RN [6]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RC TISSUE=Urinary bladder;

RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.F., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Mañan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length  
RT human and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [7]  
RP INTERACTION WITH RIPK1.  
RX MEDLINE=95277838; PubMed=7538908;  
RA Stanger B.Z., Leder P., Lee T.-H., Kim E., Seed B.;  
RA "RIP: a novel protein containing a death domain that interacts with  
RT Fas/APO-1 (CD95) in yeast and causes cell death.";  
RL Cell 81:513-523(1995).  
RN [8]  
RP INTERACTION WITH FAIM2.  
RX MEDLINE=20006292; PubMed=10535980;  
RA Somia N.V., Schmitt M.J., Vetter D.E., Van Antwerp D., Heinemann S.F.,  
RA Verma I.M.;  
RT "LFG: an anti-apoptotic gene that provides protection from fas-  
RT mediated cell death.";  
RL Proc. Natl. Acad. Sci. U.S.A. 96:12667-12672(1999).  
RN [9]  
RP STRUCTURE BY NMR OF 218-335.  
RX MEDLINE=97122332; PubMed=8967952;  
RA Huang B., Eberstadt M., Olejniczak E.T., Meadows R.P., Fesik S.W.;  
RT "NMR structure and mutagenesis of the Fas (APO-1/CD95) death domain.";  
RL Nature 384:638-641(1996).  
RN [10]  
RP VARIANT ALPS PRO-241.  
RX MEDLINE=95300225; PubMed=7540117;  
RA Fisher G.H., Rosenberg F.J., Straus S.E., Dale J.K., Middleton L.A.,  
RA Lin A.Y., Strober W., Lenardo M.J., Puck J.M.;  
RT "Dominant interfering Fas gene mutations impair apoptosis in a human  
RT autoimmune lymphoproliferative syndrome.";  
RL Cell 81:935-946(1995).  
RN [11]  
RP VARIANT ALPS TYR-260.  
RX MEDLINE=97066823; PubMed=8929361;  
RA Drappa J., Vaishnaw A.K., Sullivan K.E., Chu J.-L., Elkon K.B.;  
RT "Fas gene mutations in the Canale-Smith syndrome, an inherited  
RT lymphoproliferative disorder associated with autoimmunity.";  
RL New Engl. J. Med. 335:1643-1649(1996).  
RN [12]  
RP VARIANTS ALPS TRP-121 AND CYS-232.  
RX MEDLINE=97180145; PubMed=9028321;  
RA Bettinardi A., Brugnani D., Quiros-Roldan E., Malagoli A.,  
RA La Grutta S., Correr A., Notarangelo L.D.;  
RT "Missense mutations in the Fas gene resulting in autoimmune  
RT lymphoproliferative syndrome: a molecular and immunological  
RT analysis.";  
RL Blood 89:902-909(1997).  
RN [13]  
RP VARIANTS ALPS ASP-257 AND SER-310.  
RX MEDLINE=97180739; PubMed=9028957;  
RA Sneller M.C., Wang J., Dale J.K., Strober W., Middleton L.A., Choi Y.,  
RA Fleisher T.A., Lim M.S., Jaffe E.S., Puck J.M., Lenardo M.J.,  
RA Straus S.E.;  
RT "Clincial, immunologic, and genetic features of an autoimmune

RT lymphoproliferative syndrome associated with abnormal lymphocyte  
RT apoptosis.";  
RL Blood 89:1341-1348(1997).  
RN [14]  
RP VARIANT ALPS ALA-28.  
RX MEDLINE=97463833; PubMed=9322534;  
RA Pensati L., Costanzo A., Ianni A., Accapezzato D., Iorio R.,  
RA Natoli G., Nisini R., Almerighi C., Balsano C., Vajro P., Vegnente A.,  
RA Leviero M.;  
RT "Fas/Apol mutations and autoimmune lymphoproliferative syndrome in a  
RT patient with type 2 autoimmune hepatitis.";  
RL Gastroenterology 113:1384-1389(1997).  
RN [15]  
RP VARIANT ALPS VAL-260.  
RX MEDLINE=99038860; PubMed=9821419;  
RA Infante A.J., Britton H.A., DeNapoli T., Middleton L.A., Lenardo M.J.,  
RA Jackson C.E., Wang J., Fleisher T., Straus S.E., Puck J.M.;  
RT "The clinical spectrum in a large kindred with autoimmune  
RT lymphoproliferative syndrome caused by a Fas mutation that impairs  
RT lymphocyte apoptosis.";  
RL J. Pediatr. 133:629-633(1998).  
RN [16]  
RP VARIANTS ALPS LYS-241 AND GLN-250.  
RX MEDLINE=99192346; PubMed=10090885;  
RA Jackson C.E., Fischer R.E., Hsu A.P., Anderson S.M., Choi Y., Wang J.,  
RA Dale J.K., Fleisher T.A., Middleton L.A., Sneller M.C., Lenardo M.J.,  
RA Straus S.E., Puck J.M.;  
RT "Autoimmune lymphoproliferative syndrome with defective Fas: genotype  
RT influences penetrance.";  
RL Am. J. Hum. Genet. 64:1002-1014(1999).  
RN [17]  
RP VARIANT ALPS GLY-272.  
RX MEDLINE=99270228; PubMed=10340403;  
RA Peters A.M., Kohfink B., Martin H., Griesinger F., Wormann B.,  
RA Gahr M., Roesler J.;  
RT "Defective apoptosis due to a point mutation in the death domain of  
RT CD95 associated with autoimmune lymphoproliferative syndrome, T-cell  
RT lymphoma, and Hodgkin's disease.";  
RL Exp. Hematol. 27:868-874(1999).  
RN [18]  
RP VARIANTS ALPS ARG-82; PRO-250; GLY-260 AND ILE-270.  
RX MEDLINE=99126461; PubMed=9927496;  
RA Vaishnaw A.K., Orlinick J.R., Chu J.-L., Krammer P.H., Chao M.V.,  
RA Elkon K.B.;  
RT "The molecular basis for apoptotic defects in patients with CD95  
RT (Fas/Apo-1) mutations.";  
RL J. Clin. Invest. 103:355-363(1999).  
RN [19]  
RP VARIANTS NON-HODGKIN'S LYMPHOMA THR-25; PHE-180; LEU-183; ILE-198;  
RX VAL-260; LYS-264; LYS-272; PHE-278 AND ASN-299.  
RA Groenbaek K., Straten P.T., Ralfkiaer E., Ahrenkiel V., Andersen M.K.,  
RA Hansen N.E., Zeuthen J., Hou-Jensen K., Guldberg P.;  
RT "Somatic Fas mutations in non-Hodgkin's lymphoma: association with  
RT extranodal disease and autoimmunity.";  
RL Blood 92:3018-3024(1998).  
RN [20]  
RP VARIANTS ALPS PRO-241; VAL-260; ILE-270 AND GLY-272.  
RX MEDLINE=21311411; PubMed=11418480;  
RA Straus S.E., Jaffe E.S., Puck J.M., Dale J.K., Elkon K.B.,  
RA Roesen-Wolff A., Peters A.M.J., Sneller M.C., Hallahan C.W., Wang J.,  
RA Fischer R.E., Jackson C.M., Lin A.Y., Baeumler C., Siegart E.,  
RA Marx A., Vaishnaw A.K., Grodzicky T., Fleisher T.A., Lenardo M.J.;  
RT "The development of lymphomas in families with autoimmune  
RT lymphoproliferative syndrome with germline Fas mutations and  
RT defective lymphocyte apoptosis.";  
RL Blood 98:194-200(2001).  
CC -!- FUNCTION: Receptor for TNFSF6/FASL. The adapter molecule FADD  
CC recruits caspase-8 to the activated receptor. The resulting death-  
CC inducing signaling complex (DISC) performs caspase-8 proteolytic  
CC activation which initiates the subsequent cascade of caspases  
CC (aspartate-specific cysteine proteases) mediating apoptosis. FAS-  
CC mediated apoptosis may have a role in the induction of peripheral

Query Match 100.0%; Score 557; DB 1; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1e-41;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETVAINLSVDLSKYITTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVQL 60  
Db 218 ETVAINLSVDLSKYITTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVQL 277

QY 61 LRNWHQLHGKKEAYDTLIKDLKKANLCTLAEKIQITILKDIITSDSENSNR 111  
Db 278 LRNWHQLHGKKEAYDTLIKDLKKANLCTLAEKIQITILKDIITSDSENSNR 328

RESULT 2  
TNR6\_PIG STANDARD; PRT; 332 AA.  
AC O77736;  
DT 15-JUL-1999 (Rel. 38, Created)  
DT 15-JUL-1999 (Rel. 38, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Tumor necrosis factor receptor superfamily member 6 precursor (FASL receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen) (CD95).  
GN TNFRSF6 OR APT1 OR FAS.  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_TaxID=9823;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Bartling B., Hoffmann J., Holtz J., Schulz R., Heusch G., Darmer D.;  
RT "Expression of apoptosis-associated genes in hibernating and stunned myocardium of pig."  
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: Receptor for TNFSF6/FASL. The adaptor molecule FADD recruits caspase-8 to the activated receptor. The resulting death-inducing signaling complex (DISC) performs caspase-8 proteolytic activation which initiates the subsequent cascade of caspases (aspartate-specific cysteine proteases) mediating apoptosis. FAS-mediated apoptosis may have a role in the induction of peripheral tolerance, in the antigen-stimulated suicide of mature T-cells, or both (By similarity).  
CC -!- SUBUNIT: Binds DAXX and RIPK1 (By similarity).  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD, AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.  
CC -!- SIMILARITY: Contains 3 TNFR-Cys repeats.  
CC -!- SIMILARITY: Contains 1 death domain.

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EMBL; AJ001202; CAA04596.1; -.  
HSSP; P25445; 1DDF.  
DR InterPro; IPR000488; Death.  
DR InterPro; IPR008063; Fas\_receptor.  
DR InterPro; IPR001368; TNFR\_c6.  
DR Pfam; PF00531; death; 1.  
DR Pfam; PF00020; TNFR\_c6; 3.  
DR PRINTS; PR01680; FASRECEPTOR.  
DR SMART; SM00005; DEATH; 1.  
DR SMART; SM00208; TNFR; 3.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; 2.  
DR PROSITE; PS50050; TNFR\_NGFR\_2; 2.  
DR PROSITE; PS50017; DEATH\_DOMAIN; 1.  
KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.  
FT SIGNAL 1 16 POTENTIAL.

FT CHAIN 17 332 TUMOR NECROSIS FACTOR RECEPTOR  
FT SUPERFAMILY MEMBER 6.  
FT EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM POTENTIAL.  
FT DOMAIN 175 192 POTENTIAL.  
FT DOMAIN 193 332 CYTOPLASMIC (POTENTIAL).  
FT REPEAT 45 81 TNFR-CYS 1.  
FT REPEAT 82 125 TNFR-CYS 2.  
FT REPEAT 126 164 TNFR-CYS 3.  
FT DOMAIN 227 311 DEATH.  
FT DISULFID 46 57 BY SIMILARITY.  
FT DISULFID 58 71 BY SIMILARITY.  
FT DISULFID 61 80 BY SIMILARITY.  
FT DISULFID 83 99 BY SIMILARITY.  
FT DISULFID 102 117 BY SIMILARITY.  
FT DISULFID 105 125 BY SIMILARITY.  
FT DISULFID 127 141 BY SIMILARITY.  
FT DISULFID 144 155 BY SIMILARITY.  
FT DISULFID 147 163 BY SIMILARITY.  
FT CARBOHYD 38 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 116 N-LINKED (GLCNAC. .) (POTENTIAL).  
SQ SEQUENCE 332 AA; 37592 MW; 58B03682756BF1B CRC64;

Query Match 60.5%; Score 337; DB 1; Length 332;  
Best Local Similarity 63.1%; Pred. No. 1.7e-22;  
Matches 65; Conservative 16; Mismatches 22; Indels 0; Gaps 0;

QY 7 LSDVDLSKYITTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVQLLRNWHQ 66  
Db 221 IKDVDLGKYYITRIAEQMKITEVKDFVRKNGEETKIDEIMHDNPKDTAEQKVQLLRNWHY 280

QY 67 LHGKKEAYDTLIKDLKKANLCTLAEKIQITILKDIITSDSENSN 109  
Db 281 YHGKDAYCTLIQGLRKAKLSALADKINDIVQKDVITSEQENAN 323

RESULT 3  
TNR6\_BOVIN STANDARD; PRT; 323 AA.  
ID TNR6\_BOVIN  
AC P51867;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Tumor necrosis factor receptor superfamily member 6 precursor (FASL receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen) (CD95).  
DE TNFRSF6 OR APT1 OR FAS.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96226401; PubMed=8634151;  
RA Yoo J., Stone R.T., Beattie C.W.;  
RT "Cloning and characterization of the bovine Fas.";  
RL DNA Cell Biol. 15:227-234(1996).  
CC -!- FUNCTION: Receptor for TNFSF6/FASL. The adaptor molecule FADD recruits caspase-8 to the activated receptor. The resulting death-inducing signaling complex (DISC) performs caspase-8 proteolytic activation which initiates the subsequent cascade of caspases (aspartate-specific cysteine proteases) mediating apoptosis. FAS-mediated apoptosis may have a role in the induction of peripheral tolerance, in the antigen-stimulated suicide of mature T-cells, or both (By similarity).  
CC -!- SUBUNIT: Binds DAXX and RIPK1 (By similarity).  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD, AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.  
CC -!- SIMILARITY: Contains 3 TNFR-Cys repeats.  
CC -!- SIMILARITY: Contains 1 death domain.  
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CC -!- DISEASE: Defects in TNFRSF6 are the cause of the
CC lymphoproliferation phenotype (lpr). Lpr mice show lymphadenopathy
CC and autoantibody production.
CC -!- SIMILARITY: Contains 3 TNFR-Cys repeats.
CC -!- SIMILARITY: Contains 1 death domain.
CC -----
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M83649; AAA37593.1; -.
DR EMBL; AK002590; BAB22211.1; -.
DR EMBL; AJ295702; CAC00638.1; -.
DR EMBL; AJ295703; CAC00638.1; JOINED.
DR EMBL; AJ295704; CAC00638.1; JOINED.
DR EMBL; S56490; AAB25700.1; -.
DR EMBL; S56485; AAB25700.1; JOINED.
DR EMBL; S56486; AAB25700.1; JOINED.
DR PIR; A46484; A46484.
DR HSSP; P25445; 1DDF.
DR MGD; MGI:95484; Tnfrsf6.
DR InterPro; IPR000488; Death.
DR InterPro; IPR008063; Fas_receptor.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00020; TNFR_c6; 3.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal;
KW Disease mutation.
FT SIGNAL 1 21
FT CHAIN 22 327 TUMOR NECROSIS FACTOR RECEPTOR
FT SUPERFAMILY MEMBER 6.
FT DOMAIN 22 169 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 170 186 POTENTIAL.
FT DOMAIN 187 327 CYTOPLASMIC (POTENTIAL).
FT REPEAT 43 79 TNFR-CYS 1.
FT REPEAT 80 123 TNFR-CYS 2.
FT REPEAT 124 162 TNFR-CYS 3.
FT DOMAIN 222 306 DEATH.
FT DISULFID 44 55 BY SIMILARITY.
FT DISULFID 56 69 BY SIMILARITY.
FT DISULFID 59 78 BY SIMILARITY.
FT DISULFID 81 97 BY SIMILARITY.
FT DISULFID 100 115 BY SIMILARITY.
FT DISULFID 103 123 BY SIMILARITY.
FT DISULFID 125 139 BY SIMILARITY.
FT DISULFID 142 153 BY SIMILARITY.
FT DISULFID 145 161 BY SIMILARITY.
FT CARBOHYD 43 43 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 114 114 N-LINKED (GLCNAC. .) (POTENTIAL).
FT VARIANT 246 246 I -> N (IN LPR).
FT CONFLICT 38 38 H -> R (IN REF. 3).
SQ SEQUENCE 327 AA; 37418 MW; F6BFFC5ACE356EEE CRC64;
Query Match 50.0%; Score 278.5; DB 1; Length 327;
Best Local Similarity 50.9%; Pred. No. 2.2e-17;
Matches 57; Conservative 18; Mismatches 34; Indels 3; Gaps 1;
QY 1 ETVAINLSDVLSKYITTIAGVMTLSQVKGFVRKNGVNEAKIDEIKNDNVQDTAEQKVQL 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 210 ETIPMNASNLSLSKYIPRIAEWMTIQEAKKFARENNIKEGKIDEIMHDSIQDTAEQKVQL 269
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 61 LENWHQLHGKKEAYDTLLIKLKKANLCTLAEKIQTIILKDI---TSDSENSN 109
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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Db 270 LLCWYQSHGKSDAYQDLIKGLKKAECRRTLDKFQDMVQKDLGKSTPDTGNEN 321
RESULT 5
TNFR6 RAT
ID TNFR6 RAT STANDARD; PRT; 324 AA.
AC Q63199;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 6 precursor (FASL
DE receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen)
DE (CD95).
GN TNFRSF6 OR PT1 OR FAS.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Liver;
RX MEDLINE=94128114; PubMed=7507668;
RA Kimura K., Yamamoto M., Wakatsuki T.;
RT "A variant mRNA species encoding a truncated form of Fas antigen in
RT the rat liver.";
RL Biochem. Biophys. Res. Commun. 198:666-674 (1994).
CC -!- FUNCTION: Receptor for TNFRSF6/FASL. The adaptor molecule FADD
CC recruits caspase-8 to the activated receptor. The resulting death-
CC inducing signaling complex (DISC) performs caspase-8 proteolytic
CC activation which initiates the subsequent cascade of caspases
CC (aspartate-specific cysteine proteases) mediating apoptosis. FAS-
CC mediated apoptosis may have a role in the induction of peripheral
CC tolerance, in the antigen-stimulated suicide of mature T-cells, or
CC both (By similarity).
CC -!- SUBUNIT: Binds DAXX and RIPK1 (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
CC AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
CC -!- SIMILARITY: Contains 3 TNFR-Cys repeats.
CC -!- SIMILARITY: Contains 1 death domain.
CC -----
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CC -----
DR EMBL; D26112; BAA05108.1; -.
DR PIR; JC2395; JC2395.
DR HSSP; P25445; 1DDF.
DR InterPro; IPR000488; Death.
DR InterPro; IPR008063; Fas_receptor.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00020; TNFR_c6; 3.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
KW Receptor; Apoptosis; Glycoprotein; Transmembrane; Repeat; Signal.
FT SIGNAL 1 21 BY SIMILARITY.
FT CHAIN 22 324 TUMOR NECROSIS FACTOR RECEPTOR
FT SUPERFAMILY MEMBER 6.
FT DOMAIN 22 171 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 172 188 POTENTIAL.
FT DOMAIN 189 324 CYTOPLASMIC (POTENTIAL).
FT REPEAT 43 79 TNFR-CYS 1.
FT REPEAT 80 123 TNFR-CYS 2.
FT REPEAT 124 163 TNFR-CYS 3.
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FT DOMAIN 219 303 DEATH.
FT DISULFID 44 55 BY SIMILARITY.
FT DISULFID 56 69 BY SIMILARITY.
FT DISULFID 59 78 BY SIMILARITY.
FT DISULFID 81 97 BY SIMILARITY.
FT DISULFID 100 115 BY SIMILARITY.
FT DISULFID 103 123 BY SIMILARITY.
FT DISULFID 125 139 BY SIMILARITY.
FT DISULFID 142 154 BY SIMILARITY.
FT DISULFID 145 162 BY SIMILARITY.
FT CARBOHYD 43 43 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 114 114 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 132 132 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 324 AA; 36835 MW; D25D583C909D9D09 CRC64;

Query Match 45.0%; Score 250.5; DB 1; Length 324;
Best Local Similarity 46.4%; Pred. No. 6.2e-15;
Matches 52; Conservative 25; Mismatches 32; Indels 3; Gaps 1;

QY 1 ETVAINLSVDVLSKYITTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVQL 60
Db 207 ESVPMNVSDVNLNKYIWRTAERKMKICDAKFKARQHKIPESKIDIEHNSPQDAEQKIQL 266

QY 61 LRNWHQLHGKKEAYDTLLIKLKKANLCTLAEKIQTILKCD---ITSDSENSN 109
Db 267 LQCWYQSHGKTGACQALIQGLRKANRCIDIAEIIQAMVWEDHENSISNRNEN 318

RESULT 6
THO1_MOUSE
ID THO1_MOUSE STANDARD; PRT; 657 AA.
AC Q8R3N6; Q8BWD5; Q8BXI3;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE THO complex subunit 1 (Thol) (Nuclear matrix protein p84).
GN THO1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX TISSUE=Cerebellum, Head, Mammary gland, and Olfactory bulb;
RX MEDLINE=22354683; PubMed=12466851;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusci V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Sempile C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
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RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Breast tumor;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L.H., Shenmen C.M., Schat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: The THO/TREX complex is recruited to transcribed genes
CC and travels with the RNA polymerase during elongation. It may
CC physically link proteins that function in transcription and in RNA
CC export (By similarity).
CC -!- SUBUNIT: Part of the heteromultimeric THO/TREX complex containing
CC THO1, THO2, THO3, THO4 and NFX1/UAP56. Binds to the
CC hypophosphorylated form of RB1 (By similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear, in multiple discrete foci and
CC associated with the nuclear matrix (By similarity).
CC -!- SIMILARITY: Contains 1 death domain.
CC -!- CAUTION: Ref.1 (BAC35168) sequence differs from that shown due to
CC a frameshift in position 118.
CC
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CC -----
CC EMBL; AK031785; BAC27548.1; -.
CC EMBL; AK032200; BAC27754.1; -.
CC EMBL; AK042867; BAC31387.1; -.
CC EMBL; AK052835; BAC35168.1; ALT_FRAME.
CC EMBL; BC024951; AAH24951.1; -.
CC MGD; MGI:1919668; Thoc1.
CC InterPro; IPR000488; Death.
CC Pfam; PF00531; death; 1.
CC SMART; SM00005; DEATH; 1.
CC PROSITE; PS50017; DEATH DOMAIN; 1.
KW Transport; mRNA transport; mRNA processing; mRNA splicing;
KW Nuclear protein; Matrix protein; DNA-binding; RNA-binding.
FT DOMAIN 570 653 DEATH.
FT CONFLICT 650 650 T -> S (IN REF. 1; BAC35168).
SQ SEQUENCE 657 AA; 75436 MW; E4235E395B5A82BC CRC64;
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Query Match 14.5%; Score 81; DB 1; Length 657;
Best Local Similarity 26.5%; Pred. No. 8.8;
Matches 26; Conservative 17; Mismatches 35; Indels 20; Gaps 3;

QY 23 MTLQVKGFRKNG-----VNEAKIDEIKNDNVQDTAEQKVQLLRNWHQLHGKK 71
Db 569 ITGEQIESFANKLGEQWKILAPYLEIKDSIRQIECDSEDMKMKRAQLLVAWQDQGVH 627
QY 72 EAYDTLLIKDLKKANLCTLAEKIQTILKIDTSSENSN 109
RT "Analysis of the mouse transcriptome based on functional annotation of
```

Db	628	ATTNDNLISALNKSGLSLDAE-----SLTNDTETNS	657
RESULT 7			
RIK1_MOUSE	STANDARD;	PRT;	656 AA.
ID	Q60855; Q8CD90;		
AC	01-NOV-1997 (Rel. 35, Created)		
DT	01-NOV-1997 (Rel. 35, Last sequence update)		
DT	15-MAR-2004 (Rel. 43, Last annotation update)		
DE	Receptor-interacting serine/threonine protein kinase 2 (EC 2.7.1.37)		
DE	(Serine/threonine protein kinase RIP) (Cell death protein RIP)		
DE	(Receptor interacting protein)		
GN	RIPK1 OR RIP OR RINP.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=C57BL/6 X CBA; TISSUE=Thymus;		
RX	MEDLINE=95277838; PubMed=7538908;		
RA	Stanger B.Z.; Leder P.; Lee T.-H.; Kim E.; Seed B.;		
RA	"RIP: a novel protein containing a death domain that interacts with		
RT	Fas/APO-1 (CD95) in yeast and causes cell death.";		
RL	Cell 81:513-523(1995).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=C57BL/6J; TISSUE=Thymus;		
RX	MEDLINE=22354683; PubMed=12466851;		
RA	Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,		
RA	Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,		
RA	Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,		
RA	Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,		
RA	Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,		
RA	Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,		
RA	Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,		
RA	Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,		
RA	Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,		
RA	Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,		
RA	Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,		
RA	Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,		
RA	Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,		
RA	Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,		
RA	Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,		
RA	Sandelin A., Schneider C., Sempile C.A., Setou M., Shimada K.,		
RA	Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,		
RA	Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,		
RA	Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,		
RA	Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,		
RA	Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,		
RA	Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,		
RA	Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,		
RA	Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,		
RA	Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,		
RA	Birney E., Hayashizaki Y.;		
RT	"Analysis of the mouse transcriptome based on functional annotation of		
RT	60,770 full-length cDNAs.";		
RL	Nature 420:563-573 (2002).		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=C57BL/6; TISSUE=Brain, and Liver;		
RX	MEDLINE=22388257; PubMed=12477932;		
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,		
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,		
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,		
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,		
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,		
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,		
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,		
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,		
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,		
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,		
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,		
RA	Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,		
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,		
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,		
RA	Rodriguez A.C., Grimwood J., Schmitz J., Myers R.M.,		
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smillus D.E.,		
RA	Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;		
RT	"Generation and initial analysis of more than 15,000 full-length		
RT	human and mouse cDNA sequences.";		
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).		
CC	-!- FUNCTION: Promotes apoptosis and activation of NF-kappa-B.		
CC	-!- Required for TNFRSF1A mediated activation of NF-kappa-B.		
CC	-!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.		
CC	-!- SUBUNIT: Binds to the death domain of TNFRSF6 and TRADD. Is		
CC	recruited by TRADD to TNFRSF1A in a TNF-dependent process. Binds		
CC	RIPK3, UBCE7IP1, EGFR, IKBK, TRAF1, TRAF2 and TRAF3. Interacts		
CC	with BNLF1 (By similarity).		
CC	-!- SUBCELLULAR LOCATION: Cytoplasmic.		
CC	-!- TISSUE SPECIFICITY: Found at low levels in all tissues.		
CC	-!- INDUCTION: In Concanavalin A-treated splenocytes.		
CC	-!- PTM: Proteolytically cleaved by caspase-8 during TNF-induced		
CC	apoptosis. Cleavage abolishes NF-kappa-B activation and enhances		
CC	pro-apoptotic signaling through the TRADD-FADD interaction (By		
CC	similarity).		
CC	-!- PTM: Autophosphorylated on serine and threonine residues (By		
CC	similarity).		
CC	-!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.		
CC	-!- SIMILARITY: Contains 1 death domain.		
CC	-----		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration		
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -		
CC	the European Bioinformatics Institute. There are no restrictions on its		
CC	use by non-profit institutions as long as its content is in no way		
CC	modified and this statement is not removed. Usage by and for commercial		
CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>		
CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).		
CC	-----		
DR	EMBL; U25995; AAB60487.1; -.		
DR	EMBL; AK030959; BAC27194.1; -.		
DR	EMBL; BC050905; AAH50905.1; ALT_INIT.		
DR	EMBL; BC054542; AAH54542.1; -.		
DR	EMBL; BC058162; AAH58162.1; -.		
DR	PIR; I49299; I49299.		
DR	HSSP; P25445; 1DDF.		
DR	MGD; MGI:108212; Ripk1.		
DR	InterPro; IPR000488; Death.		
DR	InterPro; IPR000719; Prot_kinase.		
DR	InterPro; IPR008271; Ser_thr_pkin_AS.		
DR	InterPro; IPR001245; Tyr_kinase.		
DR	Pfam; PF00531; death; 1.		
DR	Pfam; PF00069; pkinase; 1.		
DR	PRINTS; PR00109; TYRKINASE.		
DR	ProDom; PD000001; Prot_kinase; 1.		
DR	SMART; SM00005; DEATH; 1.		
DR	PROSITE; PS00108; PROTEIN_KINASE_ST; 1.		
DR	PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.		
DR	PROSITE; PS50017; DEATH_DOMAIN; 1.		
KW	Transferase; Serine/threonine-protein kinase; ATP-binding;		
KW	Apoptosis.		
FT	DOMAIN 17 290 PROTEIN_KINASE.		
FT	NP_BIND 23 31 ATP (BY SIMILARITY).		
FT	BINDING 46 46 ATP (BY SIMILARITY).		
FT	ACT_SITE 138 138 BY SIMILARITY.		
FT	DOMAIN 568 654 DEATH.		
FT	VARIANT 473 473 T -> I.		
FT	CONFLICT 66 66 M -> K (IN REF. 2).		
SQ	SEQUENCE 656 AA; 74854 MW; ABB350B523879933 CRC64;		
Query Match	14.5%;	Score 80.5;	DB 1; Length 656;
Best Local Similarity	41.7%;	Pred. No. 9.7;	
Matches	20; Conservative	8; Mismatches	19; Indels 1; Gaps 1;
QY	27	QVKGFRKNGVNEAKIDEIKNDNVQDTAEQKV-QLLRNWHLHGKKEA	73





















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OM protein - protein search, using sw model

Run on: June 1, 2004, 14:35:21 ; Search time 33.2335 Seconds  
(without alignments)  
1053.831 Million cell updates/sec

Title: US-09-854-906-9  
Perfect score: 557  
Sequence: 1 ETVAINLSVDLSKYITTTA.....KIQTIIILKDITSDSENSNFR 111

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues  
Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL 25:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phase:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvirus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Query Match Length DB ID	Description
1	515	92.5 109 4 Q8IUB7	Q8iub7 homo sapien
2	510	91.6 109 4 Q8IUB6	Q8iub6 homo sapien
3	477	85.6 331 6 Q9TSN4	Q9tsn4 macaca fasc
4	472	84.7 331 6 Q9BDN0	Q9bdn0 macaca neme
5	472	84.7 333 6 Q9BDP2	Q9bdp2 macaca mula
6	465	83.5 310 6 Q9GK28	Q9gk28 macaca arct
7	465	83.5 331 6 Q9GK36	Q9gk36 macaca assa
8	458	82.2 334 6 Q9GL40	Q9gl40 macaca mula
9	457	82.0 331 6 Q9BDN4	Q9bdn4 cercocebus
10	432	77.6 319 6 Q9TV79	Q9tv79 oryctolagus
11	432	77.6 320 6 Q9XS29	Q9xs29 oryctolagus
12	426	76.5 328 6 Q9BDP0	Q9bdp0 aotus trivi
13	368	66.1 314 6 Q861W6	Q861w6 felis silve
14	328	58.9 327 6 Q97491	Q97491 ovis aries
15	186	33.4 285 13 Q9DGH7	Q9dgh7 gallus gall
16	179	32.1 312 13 Q9DGH8	Q9dgh8 gallus gall

17	100.5	18.0	481	9	Q859I9	Q859i9 staphylococ
18	96	17.2	230	5	Q9N9X2	Q9n9x2 geodia cydo
19	92.5	16.6	230	16	Q81JR7	Q81jr7 bacillus an
20	92.5	16.6	865	2	Q9XDU1	Q9xdul clostridium
21	92.5	16.6	1215	16	Q8XJ10	Q8xj10 clostridium
22	86.5	15.5	1979	5	Q96I33	Q96l33 plasmodium
23	85	15.3	1435	5	Q81IL4	Q81il4 plasmodium
24	84.5	15.2	230	16	Q814P0	Q814p0 bacillus ce
25	84	15.1	1754	5	Q812Q1	Q812q1 plasmodium
26	83	14.9	659	13	Q7ZXI7	Q7zx17 xenopus lae
27	83	14.9	709	5	Q81J73	Q81j73 plasmodium
28	82	14.7	345	3	Q9P972	Q9p972 coprinus ci
29	82	14.7	613	5	Q8IDC0	Q8idc0 plasmodium
30	81.5	14.6	185	2	P94932	P94932 mycoplasma
31	81.5	14.6	589	16	Q97FG5	Q97fg5 clostridium
32	81.5	14.6	997	16	Q89VX9	Q89vx9 bradyrhizob
33	80.5	14.5	279	2	Q7WT74	Q7wt74 marine bact
34	80.5	14.5	284	17	Q8TPL5	Q8tpl5 methanosarc
35	80	14.4	222	5	Q8IDP5	Q8idp5 plasmodium
36	79.5	14.3	1106	5	Q8IBR5	Q8ibr5 plasmodium
37	79	14.2	1132	10	Q9SFG5	Q9sfg5 arabidopsis
38	78.5	14.1	1193	4	Q92580	Q92580 homo sapien
39	78	14.0	530	16	Q8EGB5	Q8egb5 shewanella
40	78	14.0	610	5	Q9N505	Q9n505 caenorhabdi
41	77.5	13.9	572	5	Q9U0N9	Q9u0n9 plasmodium
42	77.5	13.9	591	5	Q9GU24	Q9gu24 entamoeba h
43	77.5	13.9	660	16	Q8RGT2	Q8rgt2 fuscobacteri
44	77.5	13.9	1558	5	Q96275	Q96275 plasmodium
45	77.5	13.9	1786	5	Q9U0P0	Q9u0p0 plasmodium

ALIGNMENTS

RESULT 1  
Q8IUB7  
ID Q8IUB7 PRELIMINARY; PRT; 109 AA.  
AC Q8IUB7;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE CD95 antigen (Fragment).  
GN CD95.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22404279; PubMed=12516573;  
RA Kurth J., Perniok A., Schmitz R., Iking-Konert C., Chiorazzi N.,  
RA Thompson K.M., Winkler T., Rajewsky K., Kueppers R.,  
RT "Lack of deleterious somatic mutations in the CD95 gene of  
RT plasmablasts from systemic lupus erythematosus patients and  
RT autoantibody-producing cell lines."  
RL Eur. J. Immunol. 32:3785-3792(2002).  
DR EMBL; AJ509181; CAD48931.1; --  
DR GO; GO:0007165; P:signal transduction; IEA.  
DR InterPro; IPR000488; Death.  
DR Pfam; PF00531; death; 1.  
DR SMART; SM00005; DEATH; 1.  
DR PROSITE; PS50017; DEATH\_DOMAIN; 1.  
FT NON TER 1  
SQ SEQUENCE 109 AA; 12372 MW; 5EAD927A23C0AAB8 CRC64;

Query Match 92.5%; Score 515; DB 4; Length 109;  
Best Local Similarity 100.0%; Pred. No. 2.3e-37;  
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 10 VDLSKYITTTIAGVMTLSQVKGFVRKXNGVNEAKIDEIKNDNVQDTAEQKVLRRNWHQLHG 69  
Db 1 VDLSKYITTTIAGVMTLSQVKGFVRKXNGVNEAKIDEIKNDNVQDTAEQKVLRRNWHQLHG 60

QY 70 KKEAYDTLIKDLKKNLCTLAEKIQTIILKDTSDSENSNFR 111  
Db 61 KKEAYDTLIKDLKKNLCTLAEKIQTIILKDTSDSENSNFR 102

RESULT 2  
Q8IUB6  
ID Q8IUB6 PRELIMINARY; PRT; 109 AA.  
AC Q8IUB6;  
DT 01-MAR-2003 (TReMBLrel. 23, Created)  
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)  
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)  
DE CD95 antigen (Fragment).  
GN CD95.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22404279; PubMed=12516573;  
RA Kurth J., Pernio A., Schmitz R., Iking-Konert C., Chiorazzi N.,  
RA Thompson K.M., Winkler T., Rajewsky K., Kueppers R.;  
RT "Lack of deleterious somatic mutations in the CD95 gene of  
RT plasmablasts from systemic lupus erythematosus patients and  
RT autoantibody-producing cell lines.";  
RL Eur. J. Immunol. 32:3785-3792(2002).  
DR EMBL; AJ509182; CAD48932.1; --  
DR GO; GO:0007165; P:signal transduction; IEA.  
DR InterPro; IPR000488; Death.  
DR Pfam; PF00531; death; 1.  
DR SMART; SM00005; DEATH; 1.  
DR PROSITE; PS50017; DEATH\_DOMAIN; 1.  
FT NON TER 1  
SQ SEQUENCE 109 AA; 12383 MW; D48D9C942D2044B6 CRC64;

Query Match 91.6%; Score 510; DB 4; Length 109;  
Best Local Similarity 99.0%; Pred. No. 6.3e-37;  
Matches 101; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 VDLSKYITTIAGVMTLSQVKGfVRKNGVNEAKIDEIKNDNVQDTAEQKVQLLRNWHQLHG 69  
Db 1 VDLSKYITTIAGVMTLSQVKGfVRKNGVNEAKIDEIKNDNVQDTAEQKVQLLRNWHQLHG 60

QY 70 KKEAYDTLIKDLKKNLCTLAEKIQTIILKDTSDSENSNFR 111  
Db 61 KKEAYDTLIKDLKKNLCTLAEKIQTIILKDTSDSENSNFR 102

RESULT 3  
Q9TSN4  
ID Q9TSN4 PRELIMINARY; PRT; 331 AA.  
AC Q9TSN4;  
DT 01-MAY-2000 (TReMBLrel. 13, Created)  
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)  
DE Death receptor Fas (APO-1/CD95).  
GN FAS.  
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Cercopitheciidae;  
OC Cercopitheciinae; Macaca.  
OX NCBI\_TaxID=9541;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20237686; PubMed=10773350;  
RA Murayama Y., Terao K., Inoue-Murayama M.;  
RT "Molecular cloning and characterization of cynomolgus monkey Fas.";  
RL Hum. Immunol. 61:474-485(2000).  
DR EMBL; AB031420; BAA83551.1; --  
DR HSSP; P25445; 1DDF.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.

DR GO; GO:0006915; P:apoptosis; IEA.  
DR GO; GO:0006955; P:immune response; IEA.  
DR GO; GO:0007165; P:signal transduction; IEA.  
DR InterPro; IPR000488; Death.  
DR InterPro; IPR008063; Fas receptor.  
DR InterPro; IPR001368; TNFR\_c6.  
DR Pfam; PF00531; death; 1.  
DR Pfam; PF00020; TNFR\_c6; 2.  
DR PRINTS; PR01680; FASRECEPTOR.  
DR SMART; SM00005; DEATH; 1.  
DR SMART; SM00208; TNFR; 2.  
DR PROSITE; PS50017; DEATH\_DOMAIN; 1.  
DR PROSITE; PS50050; TNFR\_NGFR\_2; 2.  
KW Receptor.  
SQ SEQUENCE 331 AA; 37265 MW; 0C617508081B05DF CRC64;

Query Match 85.6%; Score 477; DB 6; Length 331;  
Best Local Similarity 88.0%; Pred. No. 1.6e-33;  
Matches 95; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 4 AINLSVDVLSKYITTIAGVMTLSQVKGfVRKNGVNEAKIDEIKNDNVQDTAEQKVQLLRN 63  
Db 217 AINLSVDVLSKYITTIAGVMTLSQVKGfVRKNGVSEAKIDEIKNDNVQDTAEQKVQLLRN 276

QY 64 WHQLHGKKEAYDTLIKDLKKNLCTLAEKIQTIILKDTSDSENSNFR 111  
Db 277 WYQLHGKGDACDTLIKGLKTADLCTLAEKIHAVILKDTSDTENSNFR 324

RESULT 4  
Q9BDN0  
ID Q9BDN0 PRELIMINARY; PRT; 331 AA.  
AC Q9BDN0;  
DT 01-JUN-2001 (TReMBLrel. 17, Created)  
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)  
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)  
DE FAS antigen CD95.  
OS Macaca nemestrina (Pig-tailed macaque).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Cercopitheciidae;  
OC Cercopitheciinae; Macaca.  
OX NCBI\_TaxID=9545;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21383618; PubMed=11491535;  
RA Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,  
RA Weiss W.R., Ansari A.A.;  
RT "Cloning, sequencing, and homology analysis of nonhuman primate  
RT Fas/Fas-ligand and co-stimulatory molecules.";  
RL Immunogenetics 53:315-328(2001).  
DR EMBL; AF344850; AAK37610.1; --  
DR HSSP; P25445; 1DDF.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.  
DR GO; GO:0006915; P:apoptosis; IEA.  
DR GO; GO:0006955; P:immune response; IEA.  
DR GO; GO:0007165; P:signal transduction; IEA.  
DR InterPro; IPR000488; Death.  
DR InterPro; IPR008063; Fas receptor.  
DR InterPro; IPR001368; TNFR\_c6.  
DR Pfam; PF00531; death; 1.  
DR Pfam; PF00020; TNFR\_c6; 2.  
DR PRINTS; PR01680; FASRECEPTOR.  
DR SMART; SM00005; DEATH; 1.  
DR SMART; SM00208; TNFR; 2.  
DR PROSITE; PS50017; DEATH\_DOMAIN; 1.  
DR PROSITE; PS50050; TNFR\_NGFR\_2; 2.  
SQ SEQUENCE 331 AA; 37254 MW; A6CFE3DA12C94765 CRC64;

Query Match 84.7%; Score 472; DB 6; Length 331;  
Best Local Similarity 87.9%; Pred. No. 4.3e-33;  
Matches 94; Conservative 6; Mismatches 7; Indels 0; Gaps 0;





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DR Pfam; PF00531; death; 1.
DR Pfam; PF00020; TNFR_c6; 2.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS50017; DEATH DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
SQ SEQUENCE 331 AA; 37167 MW; CE58DB046C67834F CRC64;

Query Match      83.5%; Score 465; DB 6; Length 331;
Best Local Similarity 86.9%; Pred. No. 1.7e-32;
Matches 93; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 4 AINLSDVDLSKYITTTIAGVMTLSQVKGFVRKNGVNEAKIDEIKNDNVQDTAEQKVQLLRN 63
Db 217 AINLSDVDLSKYITTTIAGMTLSQVKDFVRKNGVSEAKIDEIKNDNVQDTAEQKVQLRN 276

QY 64 WHQLHGKKEAYDTLIKDLKKNLCTLAEKIQTIIILKDITSDSENSNF 110
Db 277 WYQLHGKKDADCTLIKGLKTADLCTLAEKIHAVILKDITSDTENSNF 323

RESULT 8
Q9GL40 PRELIMINARY; PRT; 334 AA.
AC Q9GL40;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Fas antigen.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA Shui B., Chi L., Zhang Y.R.;
RT "Cloning and sequencing of Rhesus monkey Fas antigen cDNA.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY007572; AAG16762.1; -.
DR HSSP; P25445; 1DDF.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000488; Death.
DR InterPro; IPR008063; Fas_receptor.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; death; 1.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS50017; DEATH DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
SQ SEQUENCE 334 AA; 37531 MW; 2DC5B1661C3191C6 CRC64;

Query Match      82.2%; Score 458; DB 6; Length 334;
Best Local Similarity 86.0%; Pred. No. 7.1e-32;
Matches 92; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 4 AINLSDVDLSKYITTTIAGVMTLSQVKGFVRKNGVNEAKIDEIKNDNVQDTAEQKVQLLRN 63
Db 220 AINLSDVDLSKYITTTIAGMTLSQVKDFGRKNGVSEAKIDEIKNDNVQDTAEQKVQLRN 279

QY 64 WHQLHGKKEAYDTLIKDLKKNLCTLAEKIQTIIILKDITSDSENSNF 110
Db 280 WYQPHGKKDADCTLIKGLKTADLCTLAEKIHAVILKDITSDTENSNF 326
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RESULT 9
Q9BDN4 PRELIMINARY; PRT; 331 AA.
AC Q9BDN4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Fas antigen CD95.
OS Cercocebus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercocebus.
OX NCBI_TaxID=9531;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21383618; PubMed=11491535;
RA Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
RA Weiss W.R., Ansari A.A.;
RT "Cloning, sequencing, and homology analysis of nonhuman primate
RT Fas/Fas-ligand and co-stimulatory molecules.";
RL Immunogenetics 53:315-328(2001).
DR EMBL; AF344843; AAK37602.1; -.
DR HSSP; P25445; 1DDF.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000488; Death.
DR InterPro; IPR008063; Fas_receptor.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00020; TNFR_c6; 2.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS50017; DEATH DOMAIN; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
FT VARIANT 44 44 I -> V.
FT VARIANT 47 47 R -> Q.
FT VARIANT 55 55 E -> D.
FT VARIANT 60 60 R -> H.
FT VARIANT 61 61 N -> S.
FT VARIANT 77 77 E -> G.
FT VARIANT 95 95 G -> A.
FT VARIANT 282 282 E -> G.
FT VARIANT 298 298 G -> D.
FT VARIANT 300 300 C -> *.
SQ SEQUENCE 331 AA; 37277 MW; 1D843C4DE1D343F4 CRC64;

Query Match      82.0%; Score 457; DB 6; Length 331;
Best Local Similarity 86.0%; Pred. No. 8.5e-32;
Matches 92; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 4 AINLSDVDLSKYITTTIAGVMTLSQVKGFVRKNGVNEAKIDEIKNDNVQDTAEQKVQLLRN 63
Db 217 AINLSDVDLSKYITTTIAGMTLSQVRDFVRKNGVSEAKIDEIKNDNVQDTAEQKVQLRN 276

QY 64 WHQLHGKKEAYDTLIKDLKKNLCTLAEKIQTIIILKDITSDSENSNF 110
Db 277 WYQLHEKKDADCTLIKGLKTAGLCTLAEKIHAVILKDITSDTENSNF 323

RESULT 10
Q9TV79 PRELIMINARY; PRT; 319 AA.
AC Q9TV79;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE B-type Fas antigen.
OS Oryctolagus cuniculus (Rabbit).
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RA Isono T., Tanbe Y., Nagano Y., Seto A.;
RT "Splicing and allelic variation in the rabbit Fas antigen gene.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB021298; BAA78430.1; -.
DR HSSP; P25445; 1DDF.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000488; Death.
DR InterPro; IPR008063; Fas receptor.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; death; 1.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
SQ SEQUENCE 319 AA; 35961 MW; 06FA0033B1846591 CRC64;

Query Match          77.6%; Score 432; DB 6; Length 319;
Best Local Similarity 75.7%; Pred. No. 1.2e-29;
Matches 84; Conservative 12; Mismatches 15; Indels 0; Gaps 0;

QY 1 ETVAINLSVDVLSKYITTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVQL 60
Db 200 EGVPMNFSVDVLSKYIPTIAEMKINEVKEFVRKNGVNEAKIDEIKNDNIQDTAEQKVQL 259

QY 61 LRNWHQLHGKKEAYDTLIKLRKANLCTLAEKIQTIILKDITSDSENSNFR 111
Db 260 LRNWHQLHGKKDAYNTLIKGLRKANLCAALAEKIQDIVQKDITSDHDNLDIR 310

RESULT 11
Q9XS29
ID Q9XS29 PRELIMINARY; PRT; 320 AA.
AC Q9XS29;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE C-type FAS antigen.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RA Isono T., Tanbe Y., Nagano Y., Seto A.;
RT "Splicing and allelic variation in the rabbit Fas antigen gene.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB021299; BAA78431.1; -.
DR EMBL; AB021296; BAA78428.1; -.
DR HSSP; P25445; 1DDF.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000488; Death.
DR InterPro; IPR008063; Fas receptor.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; death; 1.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 3.
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DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
SQ SEQUENCE 320 AA; 36102 MW; DA235E243220FFB3 CRC64;

Query Match          77.6%; Score 432; DB 6; Length 320;
Best Local Similarity 75.7%; Pred. No. 1.2e-29;
Matches 84; Conservative 12; Mismatches 15; Indels 0; Gaps 0;

QY 1 ETVAINLSVDVLSKYITTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVQL 60
Db 201 EGVPMNFSVDVLSKYIPTIAEMKINEVKEFVRKNGVNEAKIDEIKNDNIQDTAEQKVQL 260

QY 61 LRNWHQLHGKKEAYDTLIKLRKANLCTLAEKIQTIILKDITSDSENSNFR 111
Db 261 LRNWHQLHGKKDAYNTLIKGLRKANLCAALAEKIQDIVQKDITSDHDNLDIR 311

RESULT 12
Q9BDP0
ID Q9BDP0 PRELIMINARY; PRT; 328 AA.
AC Q9BDP0;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE FAS antigen CD95.
OS Aotus trivirgatus (Night monkey) (Douroucoul).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
OX NCBI_TaxID=9505;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21383618; PubMed=11491535;
RA Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
RA Weiss W.R., Ansari A.A.;
RT "Cloning, sequencing, and homology analysis of nonhuman primate
RT Fas/Fas-ligand and co-stimulatory molecules.";
RL Immunogenetics 53:315-328(2001).
DR EMBL; AF344835; AAK37531.1; -.
DR HSSP; P25445; 1DDF.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000488; Death.
DR InterPro; IPR008063; Fas receptor.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; death; 1.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
FT VARIANT 157 157 TNFR_NGFR_2; S -> T.
SQ SEQUENCE 328 AA; 37332 MW; B3DED1DAC97D6353 CRC64;

Query Match          76.5%; Score 426; DB 6; Length 328;
Best Local Similarity 78.4%; Pred. No. 4.2e-29;
Matches 87; Conservative 8; Mismatches 12; Indels 4; Gaps 1;

QY 1 ETVAINLSVDVLSKYITTIAGVMTLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVQL 60
Db 213 ETVPMNLSVDVLSKYITVIAEHMTISQVRDFVRKNGVNEAKIDEIKNDNIKDTAEQKVQL 272

QY 61 LRNWHQLHGKKEAYDTLIKLRKANLCTLAEKIQTIILKDITSDSENSNFR 111
Db 273 LRNWHQLHGKKDAYNTLIKGLRKANLTALVEKIQNIILK----DSENSNR 319

RESULT 13
Q861W6
ID Q861W6 PRELIMINARY; PRT; 314 AA.
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